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Sequence 1357, Application US/09535852
Patent No. 6638911
GENERAL INFORMATION:
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20.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 20.0
Matches 2; Conservative
  CAYATTABOG 10
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US-09-535-852-1357
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 LENGTH: 10
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Sequence 1366, Ap
Sequence 1375, Ap
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Sequence 1825, Ap
Sequence 1825, Ap
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77, Appl
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3644, Ap
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1364, Ap
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                                                                             December 29, 2004, 21:20:27 ; Search time 23.6667 Seconds (without alignments) 28.022 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-535-852-1366
US-09-535-852-1375
US-09-535-852-1395
US-09-535-852-1395
US-09-535-852-1833
US-08-737-225-77
US-08-773-225-77
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US-09-187-859-3644
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-09-839-542B-3646
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                                                                                                                                                                                                                 478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
                     Copyright
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seq length: 10
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                                                                                                                                         Perfect score:
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Result No.

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US-09-535-852-1366

Sequence 1366, Application US/09535852

Sequence 1366, Application US/09535852

Setent No. 6538911

GRERAL INFORMATION:

APPLICANT: Blachuk, Orest W.

APPLICANT: Symonds, James M.

APPLICANT: Gour, Barbara J.

ITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING

ITLE OF INVENTION: DESMOSONAL CADHERIN-MEDIATED FUNCTIONS

ITLE REPERBYCE: 100086 407C6

CURRENT PAPLICATION NUMBER: US/09/535,852

CURRENT FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 2009

SEQ ID NO 1366

LENGTH: 10
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APPLICANT: Bymonds, James M.
APPLICANT: Symonds, James M.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100086.407C.
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Length 10
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                    US-08-973-225-102
US-08-973-225-120
US-08-973-225-121
US-08-973-225-207
US-08-973-225-208
US-08-377-781A-17
US-08-377-781A-17
US-08-377-781A-18
US-09-244-298A-122
US-09-244-298A-121
US-09-516-704-122
US-09-516-704-121
US-09-187-859-834
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US-09-187-859-836
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Pred. No. 15;
0; Mismatches
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Sequence 1395, Application US/09535852
Patent No. 6638911
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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                                        ; FEATURE:
, OTHER INFORMATION: Cyclicized modulating agent comprising
, OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1366
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Facent No. 6638911

GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Bymonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: DESNOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086, 407C6
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blachuk, Orest W.
APPLICANT: Blachuk, James M.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
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Pred. No. 15;
0; Mismatches 8; Indels
                                                                                                                                           57.7%; Score 15; DB 4; Length 10; 20.0%; Pred. No. 15; 8; Indels tive 0; Mismatches 8; Indels
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CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1375
LENGTH: 10
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Sequence 1375, Application US/09535852
Patent No. 6638911
GENERAL INFORMATION:
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20.0%;
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ORGANISM: Artificial Sequence
                   ORGANISM: Artificial Sequence
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Best Local Similarity 20.0
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Symonds, James M.
TITLE OF INVENTION: CCMPOINDS AND EWTHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C6
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARES FREESE 2001-05-21
SOFTWARES FREESE 2001-05-21
SEQ ID NO 1395
LENGTH: 10
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| Sequence 1855, Application US/09535852
| Patent No. 6638911
| GENERAL INFORMATION:
| APPLICANT: Blachuk, James M. |
| APPLICANT: Gour, Barbara J. |
| TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING TITLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS SOURRENT FILLING DATE: 2001-05-21 NUMBER OF SEQ ID NOS: 2009-05-21 SOFTWARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 1225 |
| LENGTH: 10
4; Length 10;
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Pred. No. 15;
0; Mismatches
Score 15; DB 4
Pred. No. 15;
0; Mismatches
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APPLICANT: Podduturi, surecome APPLICANT: Yin, Qun TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO PITLE OF INVENTION: RECEPTOR NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSER: Glaxow Mellcome STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.8%; Score 14; DB 2; Length 10; 20.0%; Pred. No. 69; tive 0; Mismatches 8; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,640
FILING DATE: 11-DEC-1996
CLEASIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: PK3281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
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Covirla, Steven E.

Covirla, Steven E.

Duffin, David J.

Gates, Christian
Haselden, Sherril S.

Mattheakis, Larry C.

Schatz, Peter J.

Wagstrom, Christopher R.

Wrighton, Nicholas C.
                                                                                                                                                                                                                                                             Schatz, Peter J.
Balasubramanian, Palaniappan
                                                                                                                                                                                                                                                                                                                              Wagstrom, Christopher R.
Hendren, Richard W.
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   Application US/08764640
                                                                                                                                                                                                                                                                                                                                                                                           Deprince, Randolph B.
Podduturi, Surekha
                                                                                                                           Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 10 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXXXXXXXC 10
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Matches 2; Conserv
                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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US-08-973-225-77
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   Sequence 77,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Cyclicized modulating agent comprising OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion OTHER INFORMATION: recognition sequence
                                                                                                                       US-09-535-852-1829
; Sequence 1829, Application US/09535852
; Fatent NO 6619101;
; GENERAL INFOGNATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Symonds, James M.
; TITLE OF INVENTION: COMPOUNDS AND EWTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS
; FILE REPREBRICE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SEQ ID NO 1829
; LENGTH: 10
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US-09-535-852-1833
; Sequence 1833, Application US/09535852
; Pacent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TILLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TILLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TILLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
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; TILLE OF INVEN
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 20.0%;
Matches 2; Conservative
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1 CAYASTADGC 10
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Best Local Similarity
Matches 2; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-535-852-1829
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US-08-764-640-77
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APPLICANT: Dower, William J.

APPLICANT: Dower, William J.

Cwirla, Steven B.

Gates, Christian
Scharz, Peter J.

Balasubramanian, Palaniappan
Wagstrom, Christopher R.

Hendren, Richard W.

Deprince, Randolph B.

Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY N. COUNTY N. COUNTY N. COUNTY N. COUNTY N. COUNTY N. CONDUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPTRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/516,704

FILING DATE: 01-MAR-2000

CLASSIFICATION: «Unknown»

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10;
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   PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P.O. Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
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Pred. No. 69;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PK1281
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
                                                 ATTORNEY ON THE STATE OF STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Five Moore Drive, P.(
CITY: Research Triangle Park
STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 77, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.8%;
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 20.0
Matches 2; Conservative
                           CURRENT APPLICATION DATA APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-09-244-298A-77
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS:
   SOFTWARE:
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
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TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14; DB 3; Length 10;
Pred. No. 69;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: Glazo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
                              THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,225A
FILING DATE: 04-Dec.1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Five Moore Drive, P.O. Box 13398 CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 77: US-08-973-225-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 77, Application US/09244298A Patent No. 6121238
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Podduturi, Surekha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 77: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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20.0%;
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Best Local Similarity 20.0
Matches 2; Conservative
                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS ADDRESS WEL
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-244-298A-77
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Gaps

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Gaps

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Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Five Moore Drive, P.O. Box 13398
    Pred. No. 69;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 29, 2004, 21:36:43 Job time: 23.6667 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-549-090-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Research Triangle Park
                                                                                                                                                                                                                                                                               APPLICANT: Dower, william J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheaks, Larry C.
Schatz, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENČE ADDRESS:
ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                  Sequence 77, Application US/09549090 Patent No. 6465430 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 13-Apr-2000 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 919-248-1000 INFORMATION FOR SEQ ID NO: 77:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
  20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 20.0 Matches ... 2, Conservative
                        2; Conservative
                                                                   1 CXXXXXXXC 10
                                                                                                            1 CKFTIDSSSC 10
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Best Local Similarity
Matches 2; Conserva
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US-09-549-090-77
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Patent No. 6358920

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086.407C1

CURRENT APPLICATION NUMBER: US/09/187,859A

CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3646

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                           Sequence 3644, Application US/09187859A

Patent No. 6358920

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPROUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE PATENTING DATE: 2.0
SEQ ID NO 3644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-related neuronal receptor cell adhesion; OTHER INFORMATION: recognition sequence US-09-187-859-3644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
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69;
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Pred. No. 69;
0; Mismatches 8; Indels
                                                                                                                                                                           0; Mismatches
                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 77:
                                                                                                                                Score 14;
Pred. No.
    STRANDEDNESS: <Unknown>
                                                                                                                                53.8%; 20.0%;
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Best Local Similarity 20.0%;
Matches 2; Conservative (
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ORGANISM: Artificial Sequence
                                                                                                                                                                         2; Conservative
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US-09-187-859-3644
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US-09-516-704-77
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                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
                                                               APPLICATION NUMBER: US 08/973,225
APPLICATION NUMBER: US/09/549,090
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Sequence 3644, Ap Sequence 3646, Ap Sequence 1361, Ap Sequence 1370, Ap Sequence 1370, Ap Sequence 222, App Sequence 222, App Sequence 222, App Sequence 244, App Sequence 244, App Sequence 1223, Ap Sequence 1233, Ap Sequence 1233, Ap Sequence 1239, Ap Sequence 1239, Ap Sequence 1339, Ap Sequence 1339, Ap Sequence 1339, Ap Sequence 1399, Ap Sequence 1399, Ap Sequence 1399, Ap Sequence 1399, Ap Sequence 1417, Ap Sequence 1417, Ap Sequence 1451, Ap Sequence 1417, Ap Sequence 1451, Ap Sequence 1521, Ap Sequence 152

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) OTHER INFORMATION: Cyclicized modulating agent comprising ; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence US-10-654-578-1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/LOCATION OF SEQUENCE 1357, Application US/10654578

Publication No. US20040229811A1

GENERAL INFORMATION:

APPLICANT: Blachuk, James Matthew

APPLICANT: Symonds, James Matthew

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

TITLE OF INVENTION: DESMOSOWAL CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: UNDESMOSOWAL CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: 100086.407C10

CURRENT APPLICATION NUMBER: 2003-09-03

NUMBER OF SEQ ID NOS: 2009

SOFTWARE: FREESE for Windows Version 4.0

LENGTH: 10
14 US-10-083-768-77
14 US-10-395-012-3644
12 US-10-395-012-3644
12 US-10-654-578-1361
13 US-10-654-578-1361
13 US-10-654-578-1361
13 US-10-654-578-1380
13 US-10-654-578-1380
14 US-10-654-578-1380
15 US-09-214-395-220
15 US-09-572-4048-1231
15 US-09-572-4048-1231
15 US-09-572-4048-1231
15 US-09-572-4048-1231
15 US-09-572-4048-1231
15 US-09-572-4048-1335
15 US-09-572-4048-1337
15 US-09-572-4048-1417
15 US-09-572-4048-1417
15 US-09-572-4048-1417
15 US-09-572-4048-1415
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Pred. No. 1.2e+02;
0; Mismatches 8
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US-10-654-578-1366
; Sequence 1366, Application US/10654578
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ORGANISM: Artificial Sequence
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20.0%;
       Similarity 20.0
2; Conservative
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Best Local S:
Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                              December 29, 2004, 21:36:53; Search time 82 Seconds (without alignments) 43.869 Million cell updates/sec
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1: \cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: \cgn2_6/prodata/2/pubpaa/RCT_May_PUB.pep:*

3: \cgn2_6/prodata/2/pubpaa/RCT_May_PUB.pep:*

4: \cgn2_6/prodata/2/pubpaa/USO6_NEW_PUB.pep:*

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6: \cgn2_6/prodata/2/pubpaa/USO8_NEW_PUB.pep:*

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13: \cgn2_6/prodata/2/pubpaa/USO9_NEW_PUB.pep:*

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16: \cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*

17: \cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*

18: \cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*

18: \cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*

19: \cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*

10: \cgn2_6/prodata/2/pubpaa/USO0P_PUBCOMB.pep:*
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                  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-10-654-578-1366
US-10-654-578-1365
US-10-654-578-1395
US-10-654-578-1395
US-10-654-578-1825
US-10-654-578-1823
US-09-572-4048-2111
US-09-572-4048-2169
US-10-066-922-58
US-10-066-922-58
US-10-066-969-3644
US-10-066-969-3644
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Database :

Sequence:

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Searched:

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Gaps

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Result Š Length 10; 8; Indels

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RESULT 6
US-10-654-578-1825
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                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Cyclicized modulating agent comprising CHER INFORMATION: desmocollin-1 cell adhesion recognition sequence US-10-654-578-1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Cyclicized modulating agent comprising ; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence US-10-654-578-1375
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Publication No. US20040229811A1

GENERAL INFORMATION:

APPLICANT: Blachuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Gour, Barbara J.

ITLLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

ITLLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086.407C10

CURRENT APPLICATION NUMBER: US/10/654,578

CURRENT FILING DATE: 2003-09-03

NUMBER OF SEQ ID NOS: 2009

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1375
FUBLICATION NO. US20040229811A1

GENERAL INFORMATION:

APPLICANT: Blachuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: GOLI, Barbara J.

TILE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

TILLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS

TILLE REFERENCE: 100086.407C10

CURRENT APPLICATION NUMBER: US/10/654,578

CURRENT FILING DATE: 2003-09-03

NUMBER OF SEQ ID NOS: 2009

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 10
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Sequence 1385, Application US/10654578

Sequence 1385, Application US/10654578

PUBLICATION NO. US20040229811A1

GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15; DB 17; Length 10;
Pred. No. 1.2e+02;
0; Mismatches 8; Indels
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Pred. No. 1.2e+02;
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20.0%;
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 20.0%;
Matches 2; Conservative
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Best Local Similarity 20.0
Matches 2; Conservative
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| Sequence 1825, Application US/20040229811A1
| Sensent INFORMATION:
| ABPLICANT: Blachuk, Orest W. |
| APPLICANT: Symonds, James Matthew |
| APPLICANT: Gour, Barbara J. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING |
| TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS |
| TITLE OF INVENTIONS |
| TITLE OF INVEN
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| Sequence 1395, Application US/10654578
| Publication No. US20040229811A1
| GENERAL INFORMATION:
| APPLICANT: Blachuk, Orest W. | APPLICANT: Gour, Barbara J. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS TILLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS |
| TITLE OF INVENTIONS |
| TITLE OF
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Pred. No. 1.2e+02;
0; Mismatches 8; Indels
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FILE REFERENCE: 100086.407C10
CURRENT PEPLICATION NUMBER: US/10/654,578
CURRENT FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1385
LENGTH: 10
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Best Local Similarity 20.0.
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Best Local Similarity 20.0
Matches 2; Conservative
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, OTHER INFORMATION: recognition sequence US-10-654-578-1833
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20.0%;
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                                       Query Match
Best Local Similarity 20.0.
Best Local Similarity 20.0.
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Best Local Similarity 20.0
Matches 2, Conservative
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Matches 2; Conservative
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ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
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                                                         OTHER INFORMATION: Cyclicized modulating agent comprising OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion US-10-654-578-1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Cyclicized modulating agent comprising OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion OTHER INFORMATION: recognition sequence
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Publication No. US20040229811A1

GENERAL INFORMATION:

APPLICANT: Blachuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086.407C10

CURRENT FILING DATE: 2003-09-03

NUMBER OF SEQ ID NOS: 2009

SOFTWARES PRESEQ for Windows Version 4.0

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1829, Application US/10654578
Publication No. US20040229811A1
GENERAL INFORMATION
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESWOSOMAL CADHERIN-MEDIATED FUNCTIONS
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Pred. No. 1.2e+02;
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CURRENT APPLICATION NUMBER: US/10/654,578
CURRENT FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 10
  TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 20.0%;
Matches 2; Conservative
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Matches 2; Conserv
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US-10-654-578-1829
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US-10-654-578-1833
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PEATURE: OTHER INFORMATION: sequence located in C6 at 873-882 and may interact with Sequence ; OTHER INFORMATION: this patent.
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Publication No. US20030078374A1

GENERAL INFORMATION:
APPLICANT: FOR INVENTION:
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT PAPLICANT: 2000-05-17

NUMBER OF SEQ ID NOS: 4203
SEQ ID NO 2169
SEQ ID NO 2169
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE OF INVENTION: Complementary peptide ligands from the human genome
TITLE OF INVENTION: Complementary peptide ligands from the human genome
CURRENT APPLICATION NUMBER: 108/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 2111
LENGTH: 10
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Score 15; DB 17; Length 10
Pred. No. 1.2e+02;
0; Mismatches 8; Indels
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20.0%; Pred. No. 4.9e+02;
tive 0; Mismatches 8;
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Pred. No. 4.9e+02;
0; Mismatches 8
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Gaps

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OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion CHER INFORMATION: recognition sequence US-10-006-869-3646
                                                                                                                                                                                                                                                                                                                  Score 14; DB 14; Length 10;
Pred. No. 4.9e+02;
0; Mismatches 8; Indels
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CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3646
LENGTH: 10
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ADDRESSEE: Glaxo Wellcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 77, Application US/10083768 Publication No. US20030158116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hrubiec, Robert T
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20.0%;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 20.0
Matches 2; Conservative
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                                                                                                                                       TYPE: PRT
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Sequence 3644, Application US/10006869

Publication No. US20030082166A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Symonds, James Matthew

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CAMPLERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: CAMPLERIN-MEDIATED FUNCTIONS

CURRENT TILING DATE: 100086.40707

CURRENT TILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: PatentIn Ver. 2.0
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; Publication No. US20030082166A1
; GENERAL INFORMATION;
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADRENIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
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                  Sequence 58, Application US/10046922
Publication No. US2020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGRE, 3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14; DB 13; Length 10;
Pred. No. 4.9e+02;
0; Mismatches 8; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 20.0-
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                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-58
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US-10-006-869-3646
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LENGTH: 10
    US-10-046-922-58
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Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOIETIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,768
FILING DATE: 27-Feb-2002
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               Box 13398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PK3065USW TELECOMMUNICATION INFORMATION: TELEPHONE: 919-248-1000
                                                                                                                                                                                                                                        STREET: Five Moore Drive, P.O. CITY: Research Triangle Park STATE: NC
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
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                                                                                                                                                                                                                               Sequence 3644, Application US/10395032
; Sequence 3644, Application US/10395032
; Publication No. US20030229199A1
; Publication No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REPERENCE: 100086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3644
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence CEATURE: ORGANISM: Artificial Sequence CEATURE: OFFETURE: OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion CTHER INFORMATION: recognition sequence
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Best Local Similarity 20.0%; Pred. No. 4.9e+02; Matches 2; Conservative 0; Mismatches 8; Indels
                                                                                1 CXXXXXXXC 10
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US-10-395-032-3644
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0; Gaps

Search completed: December 29, 2004, 22:01:38 Job time : 83 secs

1 CXXXXXXXC 10

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1 CFTIDSSSGC 10

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 29, 2004, 21:30:17; Search time 19 Seconds (without alignments) 50.640 Million cell updates/sec Run on:

US-10-046-922-33 26 1 CXXXXXXX 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

1102 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES ouery

Description	R-phycoerythrin al	ీ.	rg mu chain v regi pallidipin - assas	hr	R-phycoerythrin ga		actin I - malaria	hemoglobin, extrac	lipopeptide WS1279	ъ.	protamine Pl - gor	- hu	glycoprotein compo	MHC H2-K-k cell su	MHC H2-L antigen -	T-cell receptor be	T-cell receptor ga	laminin B1 - weste	Na+/K+-exchanging	hypothetical TCL3	Ig heavy chain V r	mabinlin II chain	vicilin 57K chain	cadmium-binding he	acetylcholinestera	formylglycinamide	Ig H chain V-D-J r	T-cell receptor be
ΙD	A22565	151049		B22565	F22565	A33882	B45525	865726	JJ0355	C22565	137027	137263	H48394	167345	I65546	PT0652	F41946	149421	S29881	179564	PH1408	S38516	B34818	B33882	A34026	A12016	PH1602	PH0932
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venom heptapeptide hypothetical prote hypothetical L2 pr 1g heavy chain V r metallothionein is Ig H chain V-D-J r T-cell receptor be leucine-tRNA ligas acylase - Kluyvera R-phycoerythrin ga variant surface gluene Cftr protein	L-serine ammonia-1 urine glycopeptide
A58512 S08606 156695 PH1407 S59622 PH1618 PH08033 PH0934 PCI002 S19288 A37521 CG1512 157018	A25836 XGHUEU
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ALIGNMENTS

A,Title: Structural and functional analysis of the rainbow trout (Oncorbyncus mykiss) met A,Reference number: IS1049; MUID:95324545; PMID:7601121
A,Accession: IS1049
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-4 <0LS>
A,Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAAS6466.1; PID:g4379328

Query Match 34.6%; Score 9; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 2.3e+05; Matches 1; Conservative 0; Mismatches 0; Indels

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Gaps

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RESULT 3
343959
Ig mu chain V region (clone 13) - human (fragment)
C;Species: Homo sapiens (man)

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C;Accession: A33882
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant ce
A;Reference number: A94182; MUID:88016144; PMID:3477793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             actin I - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum
C;Species: 9Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Acces: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmake Mol. Biochem. Parasitol. 35, 167-176, 1989
A;Fitle: Stage-specific expression and genomic organization of the actin genes of the malarite organization organization of the malarite organization organizat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cadmium-binding pentapeptide - downy thornapple
C;Species: Datura innoxia (downy thornapple)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
                                           A,Title: Characterization of the bilin attachment sites in R-phycoerythrin. A,Reference number: A22565; MUID:85182601; PMID:3886644
A,Rocession: F22565
A,Molecule type: protein
A,Rolecule type: protein
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A;Residues: 1-5 <WES>
A;Cross-references: GB:J03988
A;Note: the authors translated the codon GAA for residue 3 as C;Comment: The actin I gene contains no introns.
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                                                                                                                                                                                                                                                                              h Similarity 100.0%; Pred. No. 2.3e+05; 1; Conservative 0; Mismatches 0; Ind
               J. Biol. Chem. 260, 4856-4863, 1985
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Best Local Similarity
Matches 1; Conserv
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A; Status: preliminary
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Spalidipin - assassin bug (fragment)
C;Species: Triatoma pallidipennis (assassin bug)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C;Accession: S55238
R;Haendlar, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin Biochem. J. 307, 465-470, 1995
A;Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib A;Reference number: S55238; MUD:95251610; PMID:7733884
A;Molecule type: protein
A;Residues: 1-4 <HAE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: B22565
B;Klotz, A.V.; Glazer, A.N.
J;Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: B22565
A;Residues: 1-5 <KLO>
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R;Queralt, R.; Oliva, R.

Gene 133, 197-204, 1993
A;Title: Identification of conserved potential regulatory sequences of the protamine-encc
A;Reference number: I37013; MUID:94040810; PMID:8224908
A;Reference number: I37027
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <a href="Residues: 1-6">RES></a>
A;Residues: 1-6 <a href="Residues: 1-6">RES></a>
A;Cross-references: EMBL:212145; NID:922910; PIDN:CAA78129.1; PID:9579612
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Cispecies: Homo sapiens (man)
Cipate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
Cipate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
Cipatession: 137263
Riwaeber, G.; Haboner, J.F.
Endocrinology 131, 2010-2015, 1992
A,Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternat A,Reference number: 137263, MuID:93010691, PMID:1396344
A,Reference number: 137263, MuID:93010691, PMID:1396344
A,Reference preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-6 <RES>
A,Foross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
Cigenetics:
A,Genetics:
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R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
B;Ochem. Mol. B;Ol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig A;Reference number: A48394; MUD:93250576; PMID:8485470
A;Reference number: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 eMAT>
A;Experimental source: milk
A;Residues: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein
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C;Species: Streptomyces willmorei
C;Species: Streptomyces willmorei
C;Species: Ox-par-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: JU0355
R;Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A;Title: Structure and synthesis of an immunoactive lipopeptide, WS1279, of microbial or A;Accession: JU0355
A;Accession: JU0355
Biochim. Blophys. Acta 1292, 273-280, 1996

Ajtille: Characterization of the constituent polypeptides of the extracellular hemoglobil Ajtille: Ajtele: Ajtele:
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A,Residues: 1-6 <TSU>
A,Residues: 1-6 <TSU>
A,Note: the structure was confirmed by synthesis
C,Keywords: blocked amino end; lipoprotein
F;1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F;1/Modified site: fatty acylated amino end (Cys) #status experimental
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C;Species: Gorilla gorilla (gorilla)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C;Accession: 137027
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Matches

ઠ 셤 Matches

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RESULT 15
167345
MHC H2-K*c cell surface glycoprotein - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C.Accession: 167345
R.Archibald, A.L.; Thompson, N.A.; Kvist, S.
EMBO J. 5, 957-965, 1986
A.;Tele: A single mucleotide difference at the 3' end of an intron causes differential standerence number: 153243; MUD:86247587; PMID:3013627
A.;Reference number: 153243; MUD:86247587; PMID:3013627
A.;Retus: pre-liminary; translated from GB/EMBL/DDBJ
A.;Molecule type: DNA
A.;Residues: 1-6 <RES
A.;Cross-references: GB:M26859; NID:g199439; PIDN:AAA39612.1; PID:g387458
C.;Genetics:
A;Introns: 6/1
C:KEywords: glycoprotein
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Search completed: December 29, 2004, 21:42:53 Job time : 20 secs

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Run on:

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P84071,
01-0CT-2004 (Rel. 45, Created)
01-0CT-2004 (Rel. 45, Last annotation update)
01-0CT-2004 (Rel. 45, Last annotation update)
Ascalin (Fragment).
Allium ascalonicum (Shallot) (Allium cepa var. aggregatum).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
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BRHP_CONIM
ID BRHP CONIM STANDARD; PRT; 7 AA.

AC P58803;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bromoheptapeptide Im.
OC Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=35631;
RN 111
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SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY
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Gapop 10.0 , Gapext 0.5
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Stevenson B., Miller J.C.; Intrachange of Lyme disease spirochete "Intra- and interbacterial genetic exchange of Lyme disease spirochete erp genes generates sequence identity amidst diversity."; J. Mol. Evol. 57:309-324 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rehm B.H.A., Ertesvag H., Valla S.;
"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-5889(1996).
EMBL, X87973; CAA61230.1;
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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1; Conservative 0; Mismatches 0; Indele
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7 AA; 849 MW; 6337244330569ED0 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, C1
01-MAR-2003 (TrEMBLrel. 23, L6
01-UUN-2003 (TrEMBLrel, 24, L6
PP-50 protein (Fragment).
Name=PF-50;
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                                                                                                                           01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-DEC-2001 (TrEMBLrel. 19,
                                                                   PRELIMINARY;
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MEDLINE=97184108; PubMed=9030520;
Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
McIntosh J.M.;
"A novel post-translational modification involving bromination of
tryptophan. Identification of the residue, L.6-bromotryptophan, in
peptides from Conus imperialis and Conus radiatus venom.";
J. Biol. Chem. 272:4689-4698(1997).
--- FUNCTION: Does not elicit gross behavioral symptoms when injected
centrally or peripherally in mice.
--- SUBCELLULAR LOCATION: Secreted.
---- IISSUE SPECIFICITY: Expressed by the venom duct.
----- ALS SPECIFICITY: Expressed by the venom duct.
----- ALS SPECIFICITY: MW=853.19; METHOD=LSI; RANGE=1-7; NOTE=Ref.1.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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MEDLINE=21171025; PubMed=11277426;
Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G
"Arabidopsis thaliana genes expressed in the early compatible interaction with root-knot nematodes.";
Mol. Plant Microbe Interact. 14:288-299(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrrolidone carboxylic acid.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ286350; CAB71014.2; -
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Hypothetical protein DiDi 10A-2b (Fragment).
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7 7 Cysteine amide.
7 AA, 795 MW; 6EA37DC6D87EA6B0 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last seq
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Q9YIQ9
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                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
MEDLINE=56198747; PubMed=8612486;
Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Detera-Wadleigh S.D.;
"Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley;
MEDLINE=96299786; PubMed=8661150;
Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;
"New variants of the human and rat nuclear hormone receptor; TR4:
expression and chromosomal localization of the human gene.";
Genomics 35:361-366(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96124520; PubMed=8560786;
Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
"Long, nearly identical untranslated sequences at the 3' terminal
regions of the genomic RNAs of cherry leafroll virus (walnut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
EMBL; Z34265; CAA84019.1; -.
NON TER 1 1 1
SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-terminus of the viral replicase (Fragment).
Cherry leaf roll virus.
            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Orphan receptor TR4-NS (Fragment).
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SEQUENCE 7 AA, 663 MW, 6DDAAB787EB05350 CRC64;
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                                                                      Rattus norvegicus (Rat)
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                                                                                                       NCBI_TaxID=10116;
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01-JUN-1998
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Dhar K., Chancock R.M., Lai C.-J.;
"Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
viral mRNA deduced from cloned complete genomic sequences.";
                                               Gaps
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=28280;
                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Influenza virus type A (Udorn/72) hemagglutinin (seg 4) cDNA, 3'
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MEDLINE=99178282; PubMed=10074533;
Crawford-Mikeza L.K., Nang R.N., Schnurr D.P.;
"Strain variation in adenovirus serotypes 4 and 7a causing acute
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.
                                               0; Indels
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Crawford-Miksza L.K.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065064; AAD03659.1; -.
NON TER 7 AA, 980 MW; 7B5EA414140322A0 CRC64;
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1; Conservative 0; Mismatches 0; Indel
Length 7;
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Last annotation update)
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NON TER 1 1 1 SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;
  DB 2; Lei
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Best Local Similarity
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SEQUENCE FROM N.A.
MEDLINE=97442476; PubMed=9295353;
MEDLINE=97442476; PubMed=9295353;
Plummer N.W., McBurney M.W., Meisler M.H.;
Plummer N.W., McBurney M.W., Meisler M.H.;
"Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
J. Biol. Chem. 272:24008-24015(1997).
EMBL; U97673; AAB8016.1; ---
GO; GO:0005216; F:ion channel activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha, Acanthopterygii, Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
                                                                                           Indels
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF487519; AAL96665.1; -.
                                               Score 9; DB 2; Length 7;
Pred. No. 1.5e+06;
0; Mismatches 0; Indele
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Extracellular fatty acid binding protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER 1 1 1
SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
7 AA; 980 MW; 7B5EA414140322A0 CRC64;
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100.0%; Pred. No.
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Human adenovirus type 7.
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
VCBI_TaxID=10519;
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STRAIN=M. T96-0620;
MEDLINE=99175281; PubMed=10074533;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease...;
J. Clin. Microbiol. 37:1107-1112(1999).
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STRAING-GOMED,
MEDLINE=99175282; PubMed=10074533;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease.";
J. Clin. Microbiol. 37:1107-1112(1999).
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STRAIN=KN T96-0620;
Crawfoord-wiksza L.K.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databages.
EMBL; AF065068; AAD03668.1; -.
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Crawford-Miksza L.K.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065065; AAD03662.1; -.
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       1; Conservative
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Matransaldolase An enzyme implicated in crab steroidogenesis.";

Matransaldolase An enzyme in call steroidogenesis.";

Matransaldolase An enzyme in call are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells.

Matransaldolase of cell motility and are ubiquitously expressed in all eukaryotic cells.

Matransaldolase of cell motility and are ubiquitously expressed in all eukaryotic cells.

Matransaldolase of cells.

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Matransaldolase in sequencing; Structural protein.
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SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
STRAIN-Clipperton Island; TISSUE-Venom;
MEDLINE=99388839; PubMed=10461743;
Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
Olivera B.M.;
A novel D-leucine-containing Conus peptide: diverse conformational
dynamics in the contryphan family.";
Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Leu-contryphan-P.
Conus purpurascens (Purple cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Canonogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carcinus maenas (Common shore crab) (Green crab).

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.

SEQUENCE.
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Mismatches
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100.0%; Pred. No. 1.5
ative 0; Mismatches
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P80709;
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Gaps
J. Pept. Res. 54:93-99(1999).
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Expressed by the venom duct.
--- TISSUE SPECIFOLITY: MW=888.4; MBTHOD=LSI; RANGE=1-8; NOTE=Ref.1.
--- SIMLARITY: Belongs to the contryphan family.
D-amino acid; Direct protein sequencing; Hydroxylation; Toxin.
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                                                                                                                                                                                                                0; Indels
                                                                                                                                                                             34.6%; Score 9; DB 1; Length 8; 100.0%; Pred. No. 1.5e+06; Live 0; Mismatches 0; Indel.
                                                                                                                              MOD_RES 4 4 D-leucine.
SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
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Adp31416
Adp31416
Adp30865

Human Human Human

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Human

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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
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                                          ABOR2561
ADP31465
ADP310654
ADP310855
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2002US - 040658BP

2002US - 040660BP

2002US - 040660BP

2002US - 040661P

2002US - 040661P

2002US - 040661P

2002US - 040664P

2002US - 040665P

2002US - 041094P

2002US - 041095P

2002US - 041095PP
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2002US-0411019P.
2002US-0411022P.
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2002US-0410961P
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29-AUG-2002;
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17-SEP-2002;
17-SEP-2002;
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ADP30533;
Adp30533 Human sec
Adp30531 Human sec
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Adp30690 Human sec
Adp31474 Human sec
Adp30793 Human sec
Adp30794 Human sec
Adp30799 Human sec
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          5.1.6
Compugen Ltd.
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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
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2002US-040658P

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2002US-0411073P.
2002US-041101P.
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2003US-0463700P.
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2003US-0463732P.
2003US-0467199P.
2003US-0467201P.
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24 CTTAAAAAC 33
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17-SSP-2002;
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17-SEP-2002;
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17-SEP-2002;
18-APR-2003;
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29-AUG-2002;
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                                                                                                                                              ADP30531;
용
                                                                                                     New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic. antifinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Behrens D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beaurang PA, Behrens D
Haishan L, Linnemann T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.2%; Score 18; DB 8; Length 89; 20.0%; Pred. No. 2.6; tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I, Chu K, Lee E, Hestir K, Beaur
RF, Huang MM, Kothakota S, Haisha
Wang Y, Wong JGP, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2531; 428pp; English.
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                                                                                                                                                                                                                                                                                                                            18-APR-2003; 2003US-0463708P.
18-APR-2003; 2003US-0463716P.
18-APR-2003; 2003US-0463716P.
02-MAY-2003; 2003US-0467201P.
02-MAY-2003; 2003US-0467201P.
02-MAY-2003; 2003US-0467203P.
19-MAY-2003; 2003US-0471336P.
19-MAY-2003; 2003US-0471336P.
22-MAY-2003; 2003US-0472420P.
22-MAY-2003; 2003US-0472420P.
09-JUN 2003; 2003US-0472430P.
               20020S-0411024P.
20020S-0411032P.
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20020S-0411041P.
20020S-0411046P.
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2003US-0476609P.
2003US-0476641P.
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2003US-0486480P.
2003US-0486891P.
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Best Local Similarity 20.0.
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                                                                                                                                                                                   17-SEP-2002; 2
17-SEP-2002; 2
17-SEP-2002; 2
17-SEP-2002; 2
17-SEP-2002; 2
17-SEP-2002; 2
11-SEP-2002; 2
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08-JUL-2003; 2
08-JUL-2003; 2
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08-JUL-2003;
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Halenbeck RF
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02-MAY-2003; 02-MAY-2003;

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Gaps

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CXXXXXXXC 10

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypoptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did form the from part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                  830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; medicine; signal transduction; glycoprotein; transcription;
                                                                                                       Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Oteuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein encoded by a full length cDNA clone SeqID 3263.
                                                                                                                                                                                                                                                  Claim 8; SEQ ID NO 3263; 1380pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 4; Length 109;
Pred. No. 2.7;
0; Mismatches 8; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL31230 standard; protein; 109 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
           08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.2
Best Local Similarity 20.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CXXXXXXXX 10
                                                                           (HELI-) HELIX RES INST
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                                                                                                                                                        WPI; 2001-524255/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo-capping method
                                                                                                                                                                        N-PSDB; AAK94457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic. anticinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule for diagnosing, preventing or treating dises such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                                 Behrens D;
                                                                                                                                                                                                                                                                                                                                             Chu K, Lee E, Hestir K, Beaurang PA, Behrens D
Huang MM, Kothakota S, Haishan L, Linnemann T;
ng Y, Wong JGP, Wu G, Zhang H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 2529; 428pp; English.
                                                                                                                                                                                                                                                                                                                 (FIVE-) FIVE PRIME THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide, SEQ ID NO: 3263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM93527 standard; protein; 109 AA
                           19-MAY-2003; 2003US-0471335P.
22-MAY-2003; 2003US-047242PP.
22-MAY-2003; 2003US-0472430P.
09-UUN-2003; 2003US-0476609P.
09-UUN-2003; 2003US-0476641P.
                                                                                                        08-JUL-2003; 2003US-0485218P.
08-JUL-2003; 2003US-0485223P.
08-JUL-2003; 2003US-0485224P.
                                                                                                                                                    08-JUL-2003; 2003US-0485325P.
14-JUL-2003; 2003US-0486446P.
14-JUL-2003; 2003US-0486480P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.2%;
                                                                                                                                                                                                     2003US-0486891P.
                                                                                                                                                                                                                      L5-JUL-2003; 2003US-0486960P.
                                                                                                                                                                                                                                 08-AUG-2003; 2003US-0493341P.
                                                                                                                                                                                                                                                                                  08-AUG-2003; 2003US-0493577P.
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                                                                                                                                                                                                                                                                  08-AUG-2003; 2003US-0493573P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             Williams LT,
Halenbeck RF,
                                                                                                                                                                                                     15-JUL-2003;
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Koga H;

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Best Local Similarity
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                                                                                                                                                  This invention relates to a novel primers useful for synthesising full length CDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                      New oligonucleotide primers (830 cDNAs) useful for synthesizing full length human cDNAs.
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Pred. No. 2.7;
0; Mismatches 8; Indels
                                                                                                                 Example 1; SEQ ID NO 3263; 1340pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein SEQ ID #1457.
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29-AUG-2002, 2002US-040658P.
29-AUG-2002, 2002US-040658P.
29-AUG-2002, 2002US-040658P.
29-AUG-2002, 2002US-040661P.
29-AUG-2002, 2002US-0406612P.
29-AUG-2002, 2002US-0406612P.
29-AUG-2002, 2002US-040664P.
29-AUG-2002, 2002US-040664P.
29-AUG-2002, 2002US-040664P.
29-AUG-2002, 2002US-040664P.
29-AUG-2002, 2002US-040664P.
29-AUG-2002, 2002US-040665P.
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2002US-0410957P.
2002US-0410958P.
2002US-0410959P.
2002US-0410960P.
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20.0%;
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17-SEP-2002; 2002US-0410947P-
17-SEP-2002; 2002US-0410948P-
17-SEP-2002; 2002US-0410949P-
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Best Local Similarity 20.0%,
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WPI; 2004-204755/20.
                  N-PSDB; ADL31229
                                                                                                                                                                                                                                                                                                                                                     Sequence 109 AA;
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17-SEP-2002;
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                                                        New
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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Halenbeck RF, Huang MM, Kothakota S, Haisha
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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                                                                                                    2002US - 0411024P

2002US - 0411032P

2002US - 0411032P

2002US - 041104FP

2002US - 0411073P

2002US - 041101P

2002US - 0411101P

2003US - 046370FP

2003US - 0472420FP

2003US - 0472420FP
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2003US-0486446P.
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17-SEP-2002;
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18-APR-2003;
18-APR-2003;
18-APR-2003;
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02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
19-MAY-2003;
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08-JUL-2003;
08-JUL-2003;
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DB 8; Length 109;

Score 18; DB (Pred. No. 2.7;

69.2**%**; 20.0**%**; S

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Pseudomonas aeruginosa
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ABO69151
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                                                                                                              Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
Gaps
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Indels
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8
Mismatches
                                                                                                  Human secreted protein SEQ ID #2241
                                                          ADP31474 standard; protein; 144 AA.
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2002US-0406608P.
2002US-0406612P.
2002US-0406612P.
2002US-0406642P.
2002US-0406642P.
2002US-0406648P.
2002US-0406646P.
2002US-0406666P.
2002US-0406666P.
2002US-0406666P.
2002US-0410944P.
2002US-0410944P.
2002US-0410949P.
2002US-0410959P.
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2002US-0411052P.
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2002US-0411073P.
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                                                                                     (first entry)
2, Conservative
                          96 CTTTTATATC 105
            CXXXXXXX 10
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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17-SEP-2002;
17-SEP-2002;
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17-SEP-2002;
17-SEP-2002;
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29-AUG-2002;
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17-SEP-2002;
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17-SEP-2002;
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                                                                       ADP31474;
Matches
                                              RESULT 6
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beaurang PA, Behrens D;
Haishan L, Linnemann T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang
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MM, Kothakota S, 1
Wong JGP, Wu G, Zh
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                                        2003US-0467201P.
2003US-0467203P.
2003US-0467230P.
2003US-0471306P.
2003US-0471336P.
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2003US 0472430P
2003US 0476619P
2003US 0485218P
2003US 0485218P
2003US 0485224P
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2003US-0486446P.
2003US-0486480P.
2003US-0486891P.
2003US-0486960P.
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Halenbeck RF, Huang MM, Koth
Pierce K, Wang Y, Wong JGP,
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2003US-0493370P.
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Halenbeck RF,
18-APR-2003;
02-MAY-2003;
02-MAY-2003;
02-MAY-2003;
19-MAY-2003;
19-MAY-2003;
22-MAY-2003;
09-JUN-2003;
09-JUN-2003;
09-JUN-2003;
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14-JUL-2003;
14-JUL-2003;
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Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
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                                                                                                                                                                                                                                                                                                                                                                                   2002US-0411052P.
2002US-0411055P.
2002US-0411003P.
2002US-041101P.
2002US-041111P.
2003US-0463700P.
2003US-0463708P.
2003US-0463708P.
2003US-0463708P.
2003US-0463708P.
2003US-0463708P.
2003US-0463708P.
2003US-0467203P.
2003US-0467203P.
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2002US-0411045P.
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2003US-0472336P.
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2003US-0476609P.
2003US-046641P.
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2003US-0493370P.
2003US-0493573P.
2003US-0493577P.
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02-MAY-2003;
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                                                                                                                                                                                                                                                                                                      7-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                      7-SEP-2002;
The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a care the ability to bind a P. aeruginosa mucleic acid, as components of effective antibacterial targets, as templates for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences or other sequences of pseudomonas species using blochip technology. Sequences ABO67926-components for aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence. Specification but was obtained in electronic format from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                        Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
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                                                                                                                 Rubenfield MJ, Nolling J, Deloughery C, Bush D
                                                                                                                                                                                                                      Disclosure; SEQ ID NO 17897; 455pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein SEQ ID #1561.
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                                                                                          (GENO-) GENOME THERAPEUTICS CORP
                                  99US-00252991.
                                                        98US-0074788P.
98US-0094190P.
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29-AUG-2002; 2002US-0406579P.
29-AUG-2002; 2002US-0406585P.
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                                                        18-FEB-1998;
27-JUL-1998;
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                                  18-FEB-1999;
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          22-APR-2003
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Matches
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       New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                          Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                           The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antichinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
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                                                                                                                                                               Score 18; DB 8; Length 171; Pred. No. 2.9;
                                                                                                                                                                                  8; Indels
                                                                                                                                                                                  0; Mismatches
                                           Claim 1; SEQ ID NO 2792; 428pp; English
                                                                                                                                                                                                                                                                                                                        Human secreted protein SEQ ID #1560
                                                                                                                                                                                                                                                                  ADP30793 standard; protein; 171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2002; 2002US-0406579F.
29-AUG-2002; 2002US-040658FP.
29-AUG-2002; 2002US-040668BP.
29-AUG-2002; 2002US-040661BP.
29-AUG-2002; 2002US-040661IP.
29-AUG-2002; 2002US-040661IP.
29-AUG-2002; 2002US-040661IP.
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2002US-0406665P.
2002US-0410946P.
2002US-0410946P.
2002US-0410947P.
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2002US-0406642P.
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2002US-0410961P.
2002US-0410962P.
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20.0%;
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                                                                                                                                                     Query Match
Best Local Similarity 20.vv,
                                                                                                                                                                                                                                                                                                     12-AUG-2004 (first entry)
                                                                                                                                                                                                                      146 CAAATAAAAC 155
                                                                                                                                                                                                    CXXXXXXX 10
                                                                                                                                              Sequence 171 AA;
                                                                                                                                                                                                                                                                                                                                                                                      WO2004035732-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2002; 2
29-AUG-2002; 2
29-AUG-2002; 2
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29-AUG-2002;
29-AUG-2002;
17-SEP-2002;
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17-SEP-2002;
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17-SEP-2002;
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X444X8X00000000X8
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beaurang PA, Behrens D;
Haishan L, Linnemann T;
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Huang MM, Kothakota S, Haisha
ng Y, Wong JGP, Wu G, Zhang H;
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Pred. No. 2.9;
0; Mismatches
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                                   2002US-0411034P.
2002US-0411032P.
2002US-0411035P.
2002US-0411037P.
2002US-0411041P.
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2002US-0411082P.
2002US-0411101P.
2002US-0411111P.
2003US-0463700P.
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2003US-0467201P.
2003US-0467203P.
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2003US-0485218P.
2003US-0485223P.
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20.0%;
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2002US-0411052P.
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Pierce K, Wang Y,
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Best Local Similarity
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17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
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02-MAY-2003;
02-MAY-2003;
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18-APR-2003;
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17-SEP-2002;
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22-MAY-2003;
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09-JUN-2003;
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8; Indels

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2003US-0467203P.
2003US-0467230P.
2003US-0471336P.
2003US-0472420P.
2003US-0472430P.
2003US-0472430P.
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2003US-0485218P.
2003US-0485218P.
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2003US-0485218P.
2003US-048546P.
2003US-048648P.
2003US-048648P.
2003US-048648P.
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2003US-048648P.
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       02-MAY-2003; 2
02-MAY-2003; 2
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                               19-MAY-2003;
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09-JUN-2003;
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08-JUN-2003;
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08-JUN-2003;
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08-AUG-2003;
08-AUG-2003;
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ABO76619
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                                                                                                                               Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                                                                Human secreted protein SEQ ID #1573
                                                            ADP30806 standard; protein; 183 AA.
                                                                                                                                                                                                                            29-AUG-2002; 2002US-0406576P.
29-AUG-2002; 2002US-040658P.
29-AUG-2002; 2002US-040658P.
29-AUG-2002; 2002US-040658P.
29-AUG-2002; 2002US-040660BP.
29-AUG-2002; 2002US-040661IP.
29-AUG-2002; 2002US-040661IP.
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29-AUG-2002; 2002US-040665P.
29-AUG-2002; 2002US-040665P.
29-AUG-2002; 2002US-040665P.
29-AUG-2002; 2002US-040666F.
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2002US-0410948P.
2002US-0410949P.
2002US-0410953P.
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2003US-0463732P.
2003US-0467199P.
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2002US-0410961P.
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2002US-0411035P.
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2002US-0411046P.
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2002US-0411055P.
2002US-0411073P.
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                                                                                              (first entry)
                 CAAATAAAAC 155
CXXXXXXX 10
                                                                                                                                                                            WO2004035732-A2.
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17-SEP-2002; 2
17-SEP-2002; 2
17-SEP-2002; 2
17-SEP-2002; 2
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18-APR-2003; 2
02-MAY-2003; 2
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17-SEP-2002; 2
17-SEP-2002; 2
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17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
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17-SEP-2002;
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                                                                                                                                                            Homo sapiens
                                                                                              12-AUG-2004
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                                                                              ADP30806;
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diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding a polypeptide which is believed to be cytostatic, antichalfammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                    New nucleic acid molecule for diagnosing, preventing or treating dise such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to an isolated nucleic acid molecule
                                                         PA, Behrens D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%; Score 18; DB 8; Length 183; 20.0%; Pred. No. 3; ive 0; Mismatches 8; Indels
                                                             Williams LT, Chu K, Lee E, Hestir K, Beaurang P.
Halenbeck RF, Huang MM, Kothakota S, Haishan L,
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa polypeptide #8794
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2804; 428pp; English.
(FIVE-) FIVE PRIME THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO76619 standard; protein; 191 AA.
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Best Local Similarity 20..
Best Local Similarity 20..
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New nucleic acid molecule for diagnosing, preventing or treating diseases
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         29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
17-SEP-2002;
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17-SEP-2002;
18-APR-2003;
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22-MAY-2003;
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17-SEP-2002;
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 The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular tragets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as tragets for artibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa caused infection, and in detection of P. aeruginosa sequences as the sequences of Pseudomonas species using biochip technology. Sequences AB067826-AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                              Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                        Rubenfield MJ, Nolling J, Deloughery C, Bush D;
                                                                                                                                                                                           Disclosure; SEQ ID NO 25365; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein SEQ ID #1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP30921 standard; protein; 228 AA
                                                                 (GENO-) GENOME THERAPEUTICS CORP
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29-AUG-2002; 2002US-0406579P.
29-AUG-2002; 2002US-040658FP.
29-AUG-2002; 2002US-0406698P.
29-AUG-2002; 2002US-0406608P.
                                98US-0074788P.
98US-0094190P.
           99US-00252991.
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                                                                                                               WPI; 2003-615309/58.
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                                                                                                                          N-PSDB; ABD10190.
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           18-FEB-1999;
                                 18-FEB-1998;
27-JUL-1998;
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Beaurang PA, Behrens D;
Haishan L, Linnemann T;
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                                                                                                                              2002US-0411037P.
2002US-0411041P.
002US-0410960P
                                                                                                 2002US-0411032P.
2002US-0411035P.
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2002US-0411082P.
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Pierce V
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Sequence 252 AA;
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                                                                                           The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antibidiammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence and is not in the specification.
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such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                     69.2%; Score 18; DB 8; Length 228; 20.0%; Pred. No. 3.1; tive 0; Mismatches 8; Indels
                                                            Claim 1; SEQ ID NO 2919; 428pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein SEQ ID #2252.
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29-AUG-2002; 2002US-040658BP.
29-AUG-2002; 2002US-040658BP.
29-AUG-2002; 2002US-040661BP.
29-AUG-2002; 2002US-040661BP.
29-AUG-2002; 2002US-040661BP.
29-AUG-2002; 2002US-040664BP.
29-AUG-2002; 2002US-040664BP.
29-AUG-2002; 2002US-0406653P.
29-AUG-2002; 2002US-0406653P.
29-AUG-2002; 2002US-0406653P.
29-AUG-2002; 2002US-0406653P.
29-AUG-2002; 2002US-0406653P.
29-AUG-2002; 2002US-0406655P.
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2002US-040658BP.
2002US-040668BP.
2002US-040661P.
2002US-0406611P.
2002US-0406612P.
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2002US-0410957P.
2002US-0410958P.
2002US-0410958P.
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2002US-0410948P.
2002US-0410949P.
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2002US-0411019P.
2002US-0411022P.
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17-SEP-2002; 2
17-SEP-2002; 2
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17-SEP-2002;
17-SEP-2002;
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                                                                                                                                                                                                                                                                    Sequence 228
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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M, Kothakota S, Haishan L, Linnemann T;
ong JGP, Wu G, Zhang H;
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                                                                                             2003US-0463700P.
2003US-0463708P.
2003US-0463716P.
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2003US-0467201P.
2003US-0467203P.
2003US-0467230P.
2003US-0471336P.
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2003US-0472430P.
2003US-0476641P.
2003US-0485218P.
2003US-048523P.
2003US-0485224P.
2003US-0485325P.
2003US-048646P.
2003US-0486480P.
2003US-0486480P.
2003US-0486891P.
2003US-0486891P.
2003US-048680P.
2003US-048680P.
2002US-0411073P.
2002US-0411082P.
2002US-0411101P.
2002US-0411111P.
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Halenbeck RF, Huang MM,
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cycostatic, antichifammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                          Beaurang PA, Behrens D
Haishan L, Linnemann T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 8; Length 258;
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                 Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Halenbeck RF, Huang MM, Kothakota S,
Pierce K, Wang Y, Wong JGP, Wu G, Zh
                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2477; 428pp; English.
                                                                                                                                                                                                                                    (FIVE-) FIVE PRIME THERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein SEQ ID #2179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP31412 standard; protein; 264 AA
            2003US-0471306P.
2003US-0471336P.
2003US-0472420P.
2003US-0476609P.
2003US-0476641P.
2003US-0485218P.
2003US-04852218P.
2003US-0485224P.
2003US-0485224P.
2003US-0485224P.
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2003US-0486960P.
2003US-0493341P.
2003US-0493370P.
2003US-0493573P.
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20.0%;
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Best Local Similarity 20.00,
Best Local 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 258 AA;
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 19-MAY-2003;
19-MAY-2003;
22-MAY-2003;
22-MAY-2003;
22-MAY-2003;
09-JUN-2003;
08-JUL-2003;
08-JUL-2003;
08-JUL-2003;
08-JUL-2003;
                                                                                                                 08-JUL-2003;
14-JUL-2003;
14-JUL-2003;
                                                                                                                                                               15-JUL-2003;
08-AUG-2003;
08-AUG-2003;
08-AUG-2003;
                                                                                                                                                                                                                                                         Williams LT,
Halenbeck RF,
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                                                                                                                                                   Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                                                                                             Human secreted protein SEQ ID #1246
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                                                      ADP30479 standard, protein, 258
                                                                                                                                                                                                                                                                                        29-AUG-2002; 2002US-0406579P.
29-AUG-2002; 2002US-040658BP.
29-AUG-2002; 2002US-040658BP.
29-AUG-2002; 2002US-04066BP.
29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406612P.
29-AUG-2002; 2002US-0406616P.
29-AUG-2002; 2002US-0406640P.
                                                                                                                                                                                                                                                                                                                                                                                              2002US-0406646P

2002US-0406653P

2002US-0406655P

2002US-0410944P

2002US-0410949P

2002US-0410949P

2002US-0410953P

2002US-0410953P

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2002US-041095P

2002US-041098P

2002US-041098P
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02-MAY-2003; 2003US-0467201P.
02-MAY-2003; 2003US-0467203P.
                                                                                                      12-AUG-2004 (first entry)
 210 CTTTTTATAC 219
                                                                                                                                                                                                            WO2004035732-A2
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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17-SEP-2002;
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17-SEP-2002;
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Gaps

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8; Indels

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29-AUG-2002; 2002US-04065959.
29-AUG-2002; 2002US-04065859.
29-AUG-2002; 2002US-04065859.
29-AUG-2002; 2002US-04066889.
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2002US-0410957P.
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17-SEP-2002; 2002US-0411022P.
17-SEP-2002; 2002US-0411023P.
17-SEP-2002; 2002US-0411032P.
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2002US-0410948P.
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17-SEP-2002; 2002US-0411111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-2002; 2002US-0411073P
28-AUG-2003; 2003WO-US026780
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17-SEP-2002; 2
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(FIVE-) FIVE PRIME THERAPEUTICS INC.

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                                                                                                                            New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                  The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antichilammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immunos, metabolic, ganetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Chu K, Lee E, Hestir K, Beaurang PA, Behrens D
Huang MM, Kothakota S, Haishan L, Linnemann T;
ng Y, Wong JGP, Wu G, Zhang H;
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he : 71.6226 secs
                                                                                                                                                                                                                  Claim 1; SEQ ID NO 3410; 428pp; English
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                                                                                     WPI; 2004-348438/32
                                                   Pierce K, Wang Y,
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      Williams LT,
Halenbeck RF,
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Sequence Sequence

Sequence Sequence Sequence

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Run on:

Sequence:

Searched:

Database

Result No.

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Sequence 23. Application US/08727688

Patent No. 5919638

GENERAL INFORMATION:
APPLICANT: Russell, John C.
TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors NUMBER OF SEQUENCES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road D377/AP6D
CITY: Abbott Park
STATE: IL
CCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%; Score 18; DB 2; Length 14;
20.0%; Pred. No. 0.17;
iive 0; Mismatches 8; Indels
         US-10-140-002-219

US-09-15A-37

US-09-15A-37

US-09-1627-650B-1

US-09-627-650B-1

US-09-436-063C-1

US-09-436-063C-1

US-09-436-063C-7

US-09-436-063C-7

US-09-627-650B-3

US-09-627-650B-3

US-09-627-650B-3

US-09-627-650B-3

US-09-627-650B-3

US-09-627-650B-3

US-09-627-650B-3

US-09-418-063-9

US-09-418-063-9

US-09-418-063-9

US-09-418-381-115

US-08-418-381-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POTEMBSK!, Priscilla E.
REGISTRATION NUMBER: 33.207
REFERENCE/DOCKET NUMBER: 5967.US.01
TELECOMMUNICATION INFORMATION:
TELEFRONE: (847) 937-0378
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/727,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FESTINGS OF SOFTWARE: FESTINGS OF SOFTWARE: FESTINGS OF SOFTWARE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: No. 5919638e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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Best Local Similarity 20.0.
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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60064
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RESULT 1
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Seguence 25096, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Appl
Sequence 17897, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-252-991A-17897

US-09-252-991A-131307

US-09-252-991A-31307

US-09-252-991A-31307

US-09-463-048A-6

US-09-60-854B-2

US-09-60-854B-2

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US-09-627-650B-5

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US-09-627-650B-5

US-09-252-991A-31728

US-09-252-991A-26112

US-09-252-991A-23050

US-09-252-991A-23050

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US-09-252-991A-31049

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US-09-252-991A-25096
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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26
1 CXXXXXXX 10
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Match Length
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1388
1497
1917
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Sequence 6, Application US/07906349A;
Retent No. 5434064
GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
TITLE OF INVENTION: TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES ANI
TITLE OF INVENTION: TARGET PROTEINS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44409, Application US/09270767

Sequence 44409, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PELING NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 44409

LENGTH: 777
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Pred. No. 0.39;
0; Mismatches 8; Indels
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Pred. No. 0.34;
0; Mismatches
             CURRENT PELICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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20.0%;
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Similarity 20.0%;
2; Conservative
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                                                                                          Sequence 17897, Application US/09252991A
Facent No. 6551795
GENERAL INFORMATION:
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPRESENCE: 107196,136
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR PILING DATE: 1999-02-18
FRIOR PILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17897
LENGTH: 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25365, Application US/09252991A

Sequence 25365, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/252,991A

FILE REPERBNCE: 10799-02-18

FILE REPERBNCE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR PEPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR PEPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR SEQIEN NUMBER: US 60/094,190

PRIOR SEQIEN OF SEQIEN NUMBER: US 60/094,190
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 0.28;
0; Mismatches
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Pred. No.
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Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
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20.0%;
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Best Local Similarity 20.0°
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Best Local Similarity 20..
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CSSSSSSAC
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TITLE OF INVENTION:
TITLE OF INVENTION:
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US-09-252-991A-25365
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                                                                                   -09-252-991A-17897
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US-09-436-063C-5

US-09-436-063C-5

Sequence 5, Application US/09436063C

Patent No. 6407210

GENERAL INFORMATION:

APPLICANT: Bander, Bruce

APPLICANT: Jorgensen, Erik

TITLE OF INVENTION: Methods Related Thereto

FILE REFERENCE: P-1095corrected

CURRENT APPLICATION NUMBER: 05/09/436,063C

CURRENT PRING DATE: 1999-11-09

PRIOR FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 5

LENGTH: 1917
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APPLICANT: Bamber, Bruce
APPLICANT: Borgensen, Erik
ITILE OF INVENTION Nemtacde Neuromuscular Junction GABA Receptors and
ITILE OF INVENTION: Methods Related Thereto
FILE REFERENCE: 21101.0009U3
CURRENT APPLICATION NUMBER: US/09/627,650B
CURRENT FILING DATE: 200-007-28
PRIOR APPLICATION NUMBER: 09/436,063
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 50
SET AND NOS: 50
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Pred. No. 0.46;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 4; Length 1497;
Pred. No. 0.44;
0; Mismatches 8; Indels
   FILE REFERENCE: GC532
CURRENT PEPLICATION NUMBER: US/09/060,854B
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASESEQ FOR Windows Version 3.0
SEQ ID NO 2
LENGTH: 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Caenorhabditis elegans
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                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-09-060-854B-2
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Best Local Similarity 20.0
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserva
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APPLICANT: EAST, Peter David
TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photor
TITLE OF INVENTION: Luminescens
FILE REFERENCE: 050179-0076
CURRENT APPLICATION NUMBER: US/09/463,048A
CURRENT APPLICATION NUMBER: PCT/AU98/00562
PRIOR PILING DATE: 1998-07-17
PRIOR FILING DATE: 1998-07-17
RIOR FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          David Aaron
Human Protease and Use of Such Protease for Pharmaceutical
Applications and for Reducing the Allergenicity of No. 6642011-H
Proteins
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Pred. No. 0.43;
0; Mismatches 8; Indels
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Pred. No. 0.39;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                         APPLICATION NUMBER: US/07/906,349A FILING DATE: 30-JUN-1992 CLASSIPRICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/643,237 FILING DATE: 18-JAN-1991 TELECHONICATION INFORMATION: TELECHONE: 202-638-5197 TELEFAX: 202-737-3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09463048A Patent No. 6630619 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 801 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.2%;
20.0%;
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Best Local Similarity 20.0%;
Matches 2; Conservative
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Best Local Similarity 20.0
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        608 CITITITIC 617
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TYPE: PRT
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LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 20.0
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Best Local Similarity 20.0
Matches 2; Conservative
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 48 amino acid
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MOLECULE TYPE: protein
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 SOFTWARE:
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                                 69.2%; Score 18; DB 4; Length 1917; 20.0%; Pred. No. 0.46; Live 0; Mismatches 8; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            Sequence 3, Application US/08824379
Patent No. 5885801
GENERAL INFORMATION:
APPLICANT: Roo. A Gururaj
TITLE OF INVENTION: High Threonine Derivatives of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/824,379
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pionneer Hi-Bred International, Inc. STREET: 700 Capital Square, 400 Locust Street CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17; DB 2;
Pred. No. 0.99;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America
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CLASSIFICATION
FUCASSIFICATION
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/459,180
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: 81mon, 80ma G.
REGISTRATION NUMBER: 37,444
REFERENCE/DOCKET NUMBER: 354-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-248-4896
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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PCT-US96-01720-9
Sequence 9, Application PC/TUS9601720
GENERAL INFORMATION:
APPLICANT:
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                                                                   Conservative
                                                                                                                                       1049 CAAATATATC 1058
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                      1 CXXXXXXXX 10
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              Query Match
Best Local Similarity
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Best Local Similarity
Matches 2; Conserva
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US-09-436-063C-5
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Sequence 20612, Application US/09252991A
Patent No. 6521795
PRERENT NO. 6521795
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
ARCHIGAGE ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION:
ARCHGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE:
107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-7
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31728
LENGTH: 150
TYPE: PRI
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Pred. No. 1.3;
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Patentin Release #1.0, Version #1.25
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                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,055
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 11,990
REFERENCE/DOCKET NUMBER: 16336-5PC
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31728, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31728
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20.0%;
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RESULT 15
US-09-252-991A-20344

; Sequence 20344, Application US/09252991A

; Sequence 20344, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICATION:
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT PILING DATE: 1099-02-18

; PRIOR PAPLICATION NUMBER: US 60/074,788

; PRIOR PAPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-02-18

; BRIOR FILING DATE: 1998-07-27

; LENGTH 1694
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20612
LENGTH: 156
                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20612
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20344
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Search completed: December 30, 2004, 13:19:18 Job time: 25.0189 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                 December 30, 2004, 13:08:04; Search time 74.5283 Seconds (without alignments) 48.267 Million cell updates/sec
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/ (cgn2_6/ptodata/1/pubpaa/US06_BVBW_PUB.pep:*
/ (cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/ (cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/ (cgn2_6/ptodata/1/pubpaa/US08_BVBCOMB.pep:*
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/cgn2_6/ptodata/l/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/l/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/l/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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26
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/cgn2_6/]
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                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                          Run on:
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	Description	Sequence 10, Appl	Sequence 7, Appli	Sequence 800, App	Sequence 28, Appl		Sequence 86, Appl	Sequence 539, App	Sequence 539, App	Sequence 20, Appl	Sequence 1851, Ap	81,	Sequence 20, Appl	Sequence 499, App
	ΩI	US-10-697-399-10	US-10-380-927-7	US-10-296-115-800	US-10-424-955A-28	US-10-437-963-162631	US-09-791-279-86	US-10-184-644-539	US-10-184-634-539	US-09-374-046A-20	US-10-102-524-1851	US-10-331-496A-81	US-10-616-263-20	US-10-123-155-499
		16	16	15	15	16	10	14	14	10	14	14	15	14
	Query Match Length DB	33	37	328	429	598	630	647	647	653	653	653	653	693
÷	Query Match	69.2	69.2	69.5	69.2	69.2	69.2	69.2	69.2	69.2	69.5	69.2	69.5	69.2
	Score	18	18	18	18	18	18	18	18	18	18	18	18	18
	Result No.	П	7	m	4	5	9	7	80	თ	10	11	12	13

; Sequence 7, Application US/10380927

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-10-146-731-49 -10-140-472-49 -10-141-761-49	-10-142-885-49 -10-158-790-49 -10-137-871-49	110-140-923-499 -10-141-756-499 -10-141-759-499 -10-140-864-499 -10-142-426-499	437-963-12 184-644-16 183-155-15 140-472-15 141-865-15 158-790-15	10 141 755 1 10 141 755 1 10 141 759 1 10 140 805 1 10 142 426 1 10 123 155 3 10 146 731 3
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ALIGNMENTS

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GENERAL INFORMATION: US20040162413A1

Sequence 10, Application US/10697399

Publication No. US20040162413A1

GENERAL INFORMATION: GETY D.

APPLICANT: Wasserot, Alain P.

APPLICANT: Marquis, David P.

APPLICANT: Marquis, David P.

TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity

FILE REPREBRUE: AME-08122

CURRENT APPLICATION NUMBER: US/10/697,399

CURRENT FILING DATE: 2003-10-30

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.2

LENGTH: 33
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                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%;
20.0%;
                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic US-10-697-399-10
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 20.0
Matches 2; Conservative
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US-10-380-927-7
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JS-10-437-963-162631
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                                                                                                                                                                                                                                                                               TYPE: PRT
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TITLE OF INVENTION: No. US20040053248Alel Nucleic Acids and Polypeptides
TITLE REFERENCE: 704PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR PRIOR TILING DATE: 2000-01-21
PRIOR PELICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 800
LENGTH: 328
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OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3
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                                      APPLICANT: Larry W. Kwak

APPLICANT: Larry W. Kwak

APPLICANT: Arya Biragyn
TITLE OF INVENTION: VIRAL CHEMOKINE-ANTIGEN FUSION PROTEINS
FILE REFERENCE: 14014.038102
CURRENT APPLICATION NUMBER: US/10/380,927
CURRENT APPLICATION NUMBER: US/10/301/29075
FRIOR FILING DATE: 2003-12-04
FRIOR APPLICATION NUMBER: 60/233,067
FRIOR PILING DATE: 2000-09-15
FRIOR FILING DATE: 2000-09-15
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence = Note OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.2%; Score 18; DB 15; Length 328;
20.0%; Pred. No. 3.1;
tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.2%; Score 18; DB 16; Length 37; 20.0%; Pred. No. 2.1;
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8-10-42-955A-28
1 Sequence 28, Application US/10424955A
2 Publication No. US20040014658A1
3 GENERAL INPORMATION:
3 APPLICANT: PROCHON BIOTECH LTD
3 APPLICANT: BOGIN, Oren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 800, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
Publication No. US20040110165A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 20.0
Matches 2; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 2; Conserva
                     GENERAL INFORMATION:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cali, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brabazuk, Brad
APPLICANT: Larbazuk, Brad
APPLICANT: See JO 16521
APPLICANT: Larbazuk, Brad
APPLICANT: La
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APPLICANT: Adar, Rivka
TITLE OF INVENTION: ACTIVE VARIANTS OF FGF WITH IMPROVED SPECIFICITY
FILE REPERENCE: 139380 IL
CURRENT APPLICATION NUMBER: US/10/424,955A
CURRENT FILING DATE: 2003-04-29
FRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 429
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Pred. No. 3.2;
0; Mismatches 8; Indels
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US-10-437-963-162631
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Pred. No. 3.4;
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APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Liula S.
APPLICANT: Lind, Peter
TITLE OF INVENTION: No. US20030050456A16
FILE REFERENCE: 00048.US1
CURRENT APPLICATION NUMBER: US/09/791,279
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Publication No. US20040123343A1
GENERAL INFORMATION:
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Publication No. US20030050456A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.2%;
Best Local Similarity 20.0%;
Matches 2; Conservative 0
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Best Local Similarity 20.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Ran, James
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT APPLICANTON EMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 539
LENGTH: 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                            Sequence 539, Application US/10184634 Publication No. US20030068684A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    T: Godowski, Paul J.
T: Gurney, Austin L.
T: Pan, James
Smith, Victoria
T: Watanabe, Colin K.
T: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 20.0
Matches 2; Conservative
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                                              288 CTTAAAAAAC 297
                                                                                                                                                                                                           APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                 Desnoyers, Luc
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          1 CXXXXXXXXC 10
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo Sapien
US-10-184-634-539
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US-09-374-046A-20
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND THE SAME
FILE REFERENCE: D3430RLC27
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 539
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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/184,715
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR PLICATION NUMBER: 60/184,606
PRIOR PLICATION NUMBER: 60/184,606
PRIOR PLICATION NUMBER: 60/184,602
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR PLICATION NUMBER: 60/184,822
PRIOR PLICATION NUMBER: 60/184,630
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PLING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
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US-10-184-644-539
Sequence 539, Application US/10184644
Publication No. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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Wood, William I.
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Pan, James
Smith, Victoria
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Best Local Similarity 20.0
Matches 2; Conservative
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Goddard, Audrey
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ORGANISM: Homo Sapien
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LENGTH: 630
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APPLICANT:
APPLICANT:
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Clark, Hilary

APPLICANT: Fechtel, Kim

APPLICANT: Genetics Institute, Inc.

TILLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REPERENCE: 00766.00103.5

CURRENT APPLICATION NUMBER: US/10/616,263

CURRENT FILING DATE: 2003-07-08

NUMBER OF SEQ ID NOS: 240

SOFTWARE: PATENTIN Ver. 2.0

LENGTH: 653

TYPE: PRT
TITLE OF INVENTION: ZEMIN, ZEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: X
; LOCATION: 114, 247, 290, 601, 604
; OTHER INFORMATION: UNKNOWN base
US-10-331-496A-81
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APPLICANT: McCOy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
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Matches 2; Conservative
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ORGANISM: Homo sapien
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APPLICANT: Gadger, Alexander
APPLICANT: Gadger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF KIDNEY CANCER
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102.524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.2%; Score 18; DB 10; Length 653; ilarity 20.0%; Pred. No. 3.5; Conservative 0; Mismatches 8; Indels
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Pred. No. 3.5;
0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1851, Application US/10102524
Publication No. US20030109434A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-331-496A-81
; Sequence 81, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
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APPLICANT: HILLAN, KENNETH J.
APPLICANT: PHILLIPS, HEIDI S.
APPLICANT: POLAKIS, PAUL
APPLICANT: SMITH VICTORIA
APPLICANT: SPENCER, SUSAN D.
APPLICANT: WILLIAMS, P. MICKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 20.0%;
Matches 2; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 2; Conserv
                                             UNSURE
(247)
                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: UNSURE
; LOCATION: (604)
US-09-374-046A-20
                                                                                                                                          UNSURE
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LOCATION:
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Gaps

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Sequence 499, Application US/10146731
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
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Pred. No. 3.5;
0; Mismatches 8; Indels
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Pred. No. 3.5;
0; Mismatches 8; Indele
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EQ ID NO 499
LENGTH: 693
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 499, Application US/10123155; Publication No. US20030068794A1; GENERAL INFORMATION:
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20.0%;
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Stewart, Timothy A
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Wood, William
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Filvaroff, Ellen
Gao, Wei-Qiang
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Best Local Similarity 20.0
Matches 2; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo Sapien
US-10-123-155-499
                                                                                                                                                             UNSURE
(601)
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NAME/KEY: UNSURE
LOCATION: (604)
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                                             (114)
                                                                                         (247)
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RESULT 14 US-10-146-731-499

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APPLICANT: "COC," LALLAGE AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C168
CURRENT APPLICATION NUMBER: US/10/140,472
CURRENT APPLICATION NUMBER: US/2-05-06
Prior Apploication removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 499
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RL323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT FILING DATE: 2002-05-15
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Pred. No. 3.5;
0; Mismatches
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Publication No. US20030138888A1
GENERAL INFORMATION:
Publication No. US20030129692A1
GENERAL INFORMATION:
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Best Local Similarity 20.0%;
Matches 2; Conservative
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Stewart, Timothy A
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Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Goddard, Audrey
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Wood, William
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Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
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Gurney, Austin L.
Sherwood, Steven
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CORGANISM: Homo Sapien
US-10-146-731-499
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-472-499
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ö 0; Gaps Query Match 69.2%; Score 18; DB 14; Length 693; Best Local Similarity 20.0%; Pred. No. 3.5; Matches 2; Conservative 0; Mismatches 8; Indels

613 CAATAAAATC 622 1 CXXXXXXXC 10 දු ද

Search completed: December 30, 2004, 13:49:59 Job time : 75.5283 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

December 30, 2004, 12:58:17 ; Search time 11.5094 Seconds (without alignments) 83.598 Million cell updates/sec Run on:

US-10-046-922-33 26 1 CXXXXXXX 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

SS	Description			_	c	cobalamin biosynth	cobalamin biosynth	hypothetical prote	probable kexin (EC	dnaK-type molecula	protein bli-4D [im	G surface protein	hypothetical prote	hypothetical prote	υ	hypothetical prote		ċ		_	_	_	hypothetical prote	hypothetical 16.7K	Ď,	pectate lyase (EC	chymotrypsin B - A		El membrane glycop	chymotrypsin (EC 3
SUMMARIES	ID	S59448	E75433	JQ1560	JC4082	AB2920	C97694	T23167	T37314	\$33575	D87803	809118	F84312	E70531	S51479	A71249	F72549	A23473	T49498	A96746	S09762	PN0103	T28088	JQ1252	T34277	A45724	S72219	A55035	~	847537
	DB	7	~	~	~	~	~	7	7	~	~	~	7	N	~	~	~	~	7	~	~	7	7	~	N	~	~	~	ч	0
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d	Query	69.2	69.2	65.4	65.4	65.4	65.4	65.4	65.4	65.4	65.4					61.5					•		61.5	•	٠	•	61.5	4	ä	61.5
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probable elongatio probable elongatio	nypountical 30.9 hypothetical prote probable yop trans probable elicitor	hypothetical prote paired-box-contain hypothetical prote	hypothetical prote RADS2 protein homo lipopolysaccharide	probable lipopolys probable glutamate	nyponnetical proce glycerol-3-phospha
G91011 A85856	123682 C71498 T00500	A84792 JE0202 T04007	T26077 S41514 C81039	C81984 T36342	A55207
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275	275 294 306 317	321 349 380	397 422 473	473	510
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ALIGNMENTS

 RESULT 1 S59448
hypothetical protein YMR206w - yeast (Saccharomyces cerevisiae) N.Alternate names hypothetical protein YM8325.07
Vibrate: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004 C;Accesion: S59448
 R;Odell, C.; Bowman, S. submitted to the EMBL Data Library, March 1995
 A;Reference number: S59441 A;Accession: S59448
 A;Molecule type: DNA A:Residues: 1-313 < ODE>
 A, Cross-references: UNIPROT: Q03695, EMBL: Z48755; NID: 9736296; PIDN: CAA88648.1; PID: 973630
 A;Experimental Bource: Btrain AB9/2 C;Genetics:
A;Gene: MIPS:YMR206w
A;Cross-references: SGD:S0004819 A;Map position: 13R
Query Match 69.2%; Score 18; DB 2; Length 313;
Hest Local Simitarity 20.0%; Pred. NO. 0.4%; Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 CXXXXXXXXC 10
 Db 245 CSSSSSAC 254

Appothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deforces radiodurans
C;Species: Deinococcus radiodurans
C;Accession: E7543
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F, W.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S; Saith, H.O.; Venter, J.C.; Fraser, C.M.
A; Reference number: A75250; MUID:20036896; PMID:10567266
A; Reference number: B7533
A; Status: Draininary
A; Molecule type: DNA
A; Residues: 1480 c.WHI>
A; Residues: Lefterences: UNIPROT:09RV87; GB:AE001963; GB:AE000513; NID:g6458869; PIDN:AAF10716
A; Experimental source: strain R1
C; Genetics:
A; Genetics:
A; Map position: 1
C; Superfamily: Deinococcus radiodurans hypothetical protein DR1142

15:01:45 2005

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Sun Jan

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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A,Reference number: AB2577; MUD:21608550; PMID:11743193

A,Status: AB2577; MUD:21608550; PMID:11743193

A,Status: Preliminary
A,Molecule type: DNA
A,Residues: 1-376 <KUR>
A,Residues: 1-376 <KUR>
A,Experimental source: strain C58 (Dupont)
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cobalamin biosynthetic protein cbiD (PA2908) [imported] - Agrobacterium tumefaciens (stra
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2233-2228, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumk A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary
A,Modecule type: DNA
A,Readiues: 1-388 cVUR>
A,Cross-references: UNIPROT:Q8UBQ6, GB:AE007869, PIDN:AAK88508.1, PID:g15158019, GSPDB:GN
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A;Experimental source: clone K01C8
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.4%; Score 17; DB 2; Length 388; Best Local Similarity 20.0%; Pred. No. 2.2; Matches 2; Conservative 0; Mismatches R: Tndale
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: AGR C 5073
A;Map position: circular chromosome
C;Superfamily: Methanobacterium cobalamin biosynthesis protein
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A;Reference number: 219702
A;Accession: T23167
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-389 <WIL>
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A;Introns: 54/2; 146/3; 208/3; 283/1; 379/3
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Cobalamin biosynthetic protein [imported] - Agrobacterium tumefaciens (strain C58, Dupon C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C; Accession: AB5920
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
                                                                                                                                                                                                                                                                                                 JQ1560

JQ1560

JQ1560

JQ1560

Mypothetical 20.6K protein - Lymantria dispar nuclear polyhedrosis virus

NyAlternate names: hypothetical protein 4

C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV

C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

R;Bjornson, R.M.; Rohrmann, G.F.

J; Gen. Virol. 73, 1499-1504, 1992

A;Title: Nucleotide sequence of the polyhedron envelope protein gene region of the Lyman A;Reference number: PQ0339; MUID:92300345; PMID:1607868

A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:Q66152; EMBL:X81051; NID:g897718; PIDN:CAA56941.1; PID:g8977 Notes: The authors translated the codon GTG for residue 161 as Leu C;Superfamily: potato virus coat protein C;Superfamily: potato virus coat protein C;Keywords: coat protein
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   Score 18; DB 2; Length 480;
Pred. No. 0.56;
0; Mismatches 8; Indels
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      69.2%;
20.0%;
Query Match
Best Local Similarity 20.0
Matches 2; Conservative
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Best Local Similarity 20.0
Matches 2; Conservative
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A,Description: involved in protein folding and assembling/disassembling of protein comple C;Superfamily: heat shock protein 70 C;Superfamily: heat shock protein 70 C;Keywords: ATP; mitochondarion; molecular chaperone; stress-induced protein F;1.23-Domain: transit peptide (mitochondrion) #status predicted <TNP> F;24-634/Product: heat shock protein 70, mitochondrial #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Durotein bii-4D [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 21-Jun-2002
C;Accession: B87803
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000, MUID: 99069613; PMID: 9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/A;Accession: D87803
A;Status: preliminary
A;Accession: D87803
A;Status: preliminary
A;Cession: D87803
A;Residues: 1-942 <ATO-A
A;Residues: 1-942 <ATO-A
A;Residues: 1-942 <ATO-A
A;Genetics: C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Accession: B08011450
A;Map position: 1
C;Superfamily: kexin; subtilisin homology
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Geneface protein 168 - Paramecium primaurelia
Geneface protein 168 - Paramecium primaurelia
Gipacias: Paramecium primaurelia
Gipacias: Paramecium primaurelia
Gipacias: Paramecium primaurelia
Gipacias: 130-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
Gipacias: 130-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
Gipacias: 151, 521-535, 1990
Airitle Conserved sequences flank variable tandem repeats in two alleles of the Genrface Airitle conserved sequences flank variable tandem repeats in two alleles of the Genrface Airitle conserved sequences: UNIPROT:P17053, EMBL:X52133; NID:g10049; PIDN:CAA36378.1; PID:g57847: Gigenetics: Cigenetics code: SGC5
Gigenetics: Code: SGC5
Giscontine and Code: SGC5
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Pred. No. 4.3;
0; Mismatches 8; Indels
                                                                                                                                                                                              65.4%; Score 17; DB 2; Length 634;
20.0%; Pred. No. 2.6;
tive 0; Mismatches 9; Indels
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Pred. No. 3;
0; Mismatches 8; Indels
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Best Local Similarity 20.0%;
Matches 2; Conservative
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A; Reference number: $78090
A; Reference number: $78090
A; Accession: $78090
A; Molecule type: DNA
A; Residues: 1-460, 481-500, 'QGEREIASENQIRGEFDLSG', 501-634 <SMI>
A; Residues: 1-460, 481-500, 'QGEREIASENQIRGEFDLSG', 501-634 <SMI>
A; Residues: 1, 460, 481-500, 'QGEREIASENQIRGEFDLSG', 501-634 <SMI>
B; Searle, S.; Campos, A.J.R.; Coulson, R.M.R.; Spithill, T.W.; Smith, D.F.
Nucleic Acids Res. 17, 5081-5095, 1989
A; Title: A family of heat shock protein 70-related genes are expressed in the promastigc A; Reference number: $05438; MUID:89345072; PMID:2762121
                                                                                                                                                                                                                                                                                                                   probable kexin (EC 3.4.21.61) - Caenorhabditis elegans (fragment)
N;Alternate names: blisterase 4
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T37314
E;Thacker, C; Peters, K.; Srayko, M.; Rose, A.M.
Gene, 9, 956-971, 1995
A;Title: The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/su
A;Reference number: Z21679; MUID:95293228; PMID:7774813
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N;Alternate names: heat shock protein 70-related protein; mitochondrial stress protein
C;Species: Leishmania major
C;Date: 09-Dec-1997 #eequence revision 09-Dec-1997 #text_change 09-Jul-2004
C;Accession: S33575; S78090; S05438
R;Searle, S,;McCrossan, M.V.; Snith, D.F.
J. Cell Sci. 104, 1091-1100, 1993
A;Title: Expression of a mitochondrial stress protein in the protozoan parasite Leishman
A;Reference number: S33575; MUID:93300981; PMID:8314893
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-570 <TTRA>
A;Cross-references: EMBL:L29440; NID:g459702; PIDN:AAA98752.1; PID:g459703
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Pred. No. 2.5;
0; Mismatches 8; Indels
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C;Keywords: alternative splicing; hydrolase; serine proteinase
                                        Indels
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8
          Pred. No. 2.2;
0; Mismatches
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A;Residues: 1-634 <SEA>
A;Cross-references: UNIPROT:P12076; EMBL:X64137
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nilarity 20.0%;
Conservative
      20.08;
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      Best Local Similarity 20.0
Matches 2; Conservative
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Best Local Similarity
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Match 61.5%; Score 16; DB 2; Length 105; Local Similarity 20.0%; Pred. No. 5.8; es 2; Conservative 0; Mismatches 8; Indels
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Best Local Similarity 20.0%;
Matches 2; Conservative
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Cispeciaes: Mycobacterium tuberculosis
Cispeciaes: Mycobacterium tuberculosis
Cispeciaes: Mycobacterium tuberculosis
Cibate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
CiAccession: E70531

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reterence number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70531
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-85 <COL>
A;Cross-references: UNIPPROT:007207; GB:296072; GB:AL123456; NID:g3261793; PIDN:CAB09466.
A;Experimental source: strain H37Rv
C;Genetics:
A;Genetics:
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$51479
drought-induced protein Di21 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 15-Jul-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
R;Gosti, F.; Bertauche, N.; Vartanian, N.; Giraudat, J.
Nod. Gen. Genet. 246, 10-18, 1995
A;Title: Abscisic acid-dependent and -independent regulation of gene expression by programative of the sequence of shown; translation not shown
A;Accession: S51479
A;Status: nucleic acid sequence not shown; translation not shown
                        C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Date: 02-Reb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C; Date: 02-Reb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C; Ridg, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freites, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; LiA; Reference number: A84160; MulD:20504483; PMID:11016950
A; Reterence number: A84160; MulD:20504483; PMID:11016950
A; Residues: preliminary
A; Residues: 1-71 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1771 <STO>
A;Cross-references: UNIPROT:Q9HPK1; GB:AE004437; NID:g10581076; PIDN:AAG19866.1; GSPDB:G
C;Genetics
A;Gene: VNG1598H
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hypothetical protein Vng1598h [imported] - Halobacterium sp. NRC-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16; DB 2; Length 71;
Pred. No. 5.1;
0; Mismatches 8; Indels
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20.0%;
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Best Local Similarity 20.0
Matches 2; Conservative
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Best Local Similarity 20.0
Matches 2; Conservative
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Gaps

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A;Molecule type: mRNA
A;Residues: 1-104 <GOS>
A;Cross-references: UNIPROT:Q39084; EMBL:X78S85; NID:g469111; PIDN:CAA55322.1; PID:g46911
A;Cross-references: UNIPROT:Q39084; EMBL:X78S85; NID:g469111; PIDN:CAA55322.1; PID:g46911
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
C;Genetics:
A;Gene: Di21
C;Superfamily: late embryogenesis-abundant protein leas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: A71249
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. S, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic an
A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross_references: UNIRROT:057986; GB:AP000001; NID:g3236128; PIDN:BAA29320.1; PID:g3256
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Pred. No. 5.8;
0; Mismatches 8; Indels
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15:01:45 2005
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Run on:

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O.T.MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO000001657 (Fragment).
Name-ENSANGSO0000001397;
Anopheles gambiae str. PEST.
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20.0%;
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Q7PRQ7;
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Matches
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1D Q7PRQ
AC 07PRQ
DT 01-M
DT 01-M
DT 01-M
DT 01-M
GN Names
OS Anopl
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Q96KM3
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Q03695 saccharomyc
Q62df4 cryza sativ
Bad0932 oryza sativ
Q81x87 deinococcus
Q81x86 home sapien
Q81pd6 hordeum vul
Q961j4 homo sapien
Q661j4 homo sapien
Q661j4 homo sapien
Q661j4 homo sapien
Q661j6 oryza sativ
Q6525 grippidium m
Q66yes2 oryza sativ
Q6523 oryza sativ
Bad10719 oryza sativ
Q6523 oryza sativ
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Q7pyi3 anopheles g
Q21081 caenorhabdi
Q9vmg7 drosophila
Q7x34 oryza sativ
Cae64361 oryza sat
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P12076 leishmania
Q819p8 corbicula f
Aao17927 corbicula
Q9nke3 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96km3 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                               December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds (without alignments) 62.362 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                        1825181 segs, 575374646 residues
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Q70RD3
Q70RD3
CAD87007
CBID AGRTS
Q721081
Q921081
Q921081
Q7X7A4
Q7X7A4
Q7X7A4
Q803D5
HS71 LEIMA
Q819P8
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Q819P8
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07PRQ7

YM58 YEAST

06ZDR4

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Maximum Match 100%
Listing first 45 summaries
                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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ReBult Š.

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                                                            Q9h1v5 homo sapien
Occid yarrowia 11
P17053 paramecium
Q94710 paramecium
Q76973 paramecium
A894225 paramecium
G6192 neisseria g
A8816526 neisseria g
A8816526 neisseria g
Q9hx1 halobacteri
Q9hx1 halobacteri
hepatitis b
caenorhabdi
anopheles g
homo sapien
yarrowia li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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  Q80gv2
P51559
Q7qe80
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Pred. No. 0.66;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEALY, DESCUES, WW DOWAIN 1; 2.
PROSITE; PSS0020; WW DOWAIN 2; 2.
SEQUENCE 213 AA; Z3868 MW; A21054FF8214CC7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         096KM3 PRELIMINARY; PRT; 213 AA. 096KM3; Ol-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DAR-2003 (TrEMBLrel. 19, Last annotation update) Aberran kW domain-containing oxidoreductase. Name-WWOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 98:11417-11422 (2001).

EMBL, AF325423; AAL05451.1; -...

EMBL, AF325424; AAL05451.1; JOINED.

EMBL, AF325424; AAL05451.1; JOINED.

EMBL, AF325426; AAL05451.1; JOINED.

EMBL, AF325426; AAL05451.1; JOINED.

EMBL, AF325425; AAL05451.1; JOINED.
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             BLI4 CAEEL
                                                            09H1V5
06CCI6
G168 PARPR
094710
06P0K6
AAS94225
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AAS16526
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InterPro: , IPROJ1202; WW_RepS_WWP.
Pfam; PF00397; WW; 2.
SWART; SM00456; WW; 2.
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Gaps

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Putative transcription factor Myb protein.

Name=P0481P05.20;

Oryza sativa (japonica cultivar-group).

Bukaryota, Viridiplanies; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Nort machines
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Boprmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.2%; Score 18; DB 2; Length 357; 20.0%; Pred. No. 0.81;
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Pred. No. 0.81;
    Indels
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Submitred (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP004376; BAD03322.1;
SEQUENCE 357 AA; 36754 MW; 3F4F56860D3B4E22 CRC64;
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Last annotation update)
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    Mismatches
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                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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02-MAR-2004 (TrEMBLrel. 27, Last seg
02-MAR-2004 (TrEMBLrel. 27, Last ann
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SM053TE; PS000037; MYB 1; UNKNOWN 1.
PROSITE; PS00034; MYB 2; 1.
PROSITE; PS00090; MYB 3; 2.
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20.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein.
SEQUENCE 357 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P0481F05.20.
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BAD09322;
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Matches
    Matches
                                                                                                                                                                     RESULT 4
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
MEDLINE=97313268; PubMed=9169872;
MEDLINE=973131268; PubMed=9169872;
MEDLINE=973131268; PubMed=9169872;
Connor R., Churcher C.M., Badcock K., Brown D., Chillingworth T., Gonnor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical 35.0 kDa protein in PFK2-HFA1 intergenic region.
OrderedLocusNames=YMR206W; ORFNames=YM8325.07;
Saccharomyces cerevisiae (Baker's spassl).
Bukaryota; Fungi; Asomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetes.
                                                                                                                                          Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 2; Length 283;
Pred. No. 0.74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                      283 AA; 25479 MW; EF5695E19584D5F2 CRC64;
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Pred. No. 0.77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                               EMBL; AAAB01008847; EAA06779.2; -.
InterPro; IPR000877; Prot inh BBI.
PROSITE; PS00281; BOWMAN BIRK; UNKNOWN_2.
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Poly-Gln.
Poly-Ser.
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-!- SIMILARITY: SOME, TO YEAST YNR014W.
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20.0%;
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20.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 CASSSSTTSC 172
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GermOnline; 142881; -.
SGD; S0004819; YMR206W.
Hypothetical protein.
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                                                                                                                                                                                                                                             preliminary data.
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246 2
313 AA;
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nes 2; Conserv
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                                                                                              SEQUENCE FROM N.A. STRAIN=PEST;
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AC 003659;
DT 01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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5750 MW;
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                                                                                                                                                                                                         and mouse cDNA sequences.
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Matches 2; Conservative
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nes 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 AA;
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SEQUENCE
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Q8LPD6
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Maruslina K., Farmer A.A., Rubin G.M., Hong L.,
Staplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L.A.; Utterback T.R., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 2; Length 480;
Pred. No. 0.91;
                                                                                                                                                                                                                                                                                                                                                      Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; DR1142; -.
Complete proteome; Hypothetical protein.
SEQUENCE 480 AA; 49364 MW; 18B962ADA5CA24AE CRC64;
                                                                                                                                                                                                                      01-MAY_2000 (TrEMBLrel. 13, Created)
01-MAY_2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein DR1142.
OrderedLocusNames=DR1142;
Deinococcus radiodurans.
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Last annotation update)
8
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 286:1571-1577(1999).
EMBL; AE001963; AAF10716.1; -.
PIR; E75433; E75433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.2%;
20.0%;
                                                                                                                                                                                                                                                                                                                                                                         Deinococcaceae; Deinococcus.
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Best Local Similarity 20.00,
2; Conservative
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                                                                             322 ČSATASASSČ 331
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M.;
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Matches
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1D 0081XM
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Kroyminski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baldwin A., "The effect of thiocarbamate herbicides and the safener dichlormid in "The effect of thiocarbamate herbicides and the safener dichlormid in barley and wild oats."; Thesis (2001), Department of Cardiff School of Biosciences, Cardiff university, Cardiff, United Kingdom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vilgare (Barley).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO1297; HTHFFis.
PRINTS; PR01590; HTHFIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Baldwin A., Harwood J.L., Machray G.C., Francis D., Rogers H.J.;
Submitred (OCT-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; AJ419772; CAD11963.1;
HSSP; P12653; 1AXD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 2; Length 52;
Pred. No. 1.9;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7392EB72A3C70B9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Putative glutathione-S-transferase (Fragment)
                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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us-10-046-922-33.rup

096LJ4

RESULT 9

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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OJ1118_A06.7-1.
0J1118_A06.7-1.
0J118_A06.7-1.
Sheriat (Japonica cultivar-group).
Eukaryota, Viridiplantaes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEWBLrel. 27, Created)
05-JUL-2004 (TrEWBLrel. 27, Last sequence update)
05-JUL-2004 (TrEWBLrel. 27, Last sequence update)
05-JUL-2004 (TrEWBLrel. 27, Last annotation update)
Hypothetical protein OJ1119_C03.6.
Name=OJ1119_C03.6,
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
NNBL_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
clone:OJII18 A06.";
Submitted (JŪL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003873; BAD08805.1; -.
Hypothetical protein.
SEQUENCE 139 AA; 14109 MW; E281360370FB63C9 CRC64;
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EMBL, APOOS969; BAD26467.1; -.
SEQUENCE 155 AA, 16233 MW; 02DB36E5E8C77B52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h Similarity 20.0%; Pred. No. 2.7; 2; Conservative 0; Mismatches 8; Indels
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Best Local Similarity 20.0%; Pred. No. 2.8;
Matches 2; Conservative 0; Mismatches
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                                                                                                                                                          139 AA
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01-JUN-2003 (TrEMBLrel. 24, Created)
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                                                                                                                                                          PRELIMINARY;
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77 CAAITSSSSC 86
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=39947;
                                                                                                                                                          BAD08805
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AC 08
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name=0J1118_A06.7-1;
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Mintartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugano S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO58166; BAB71697.1;
GO; GO:0005243; F:ATP binding; IEA.
GO; GO:0005740; F:transferase activity; IEA.
GO; GO:0006748; F:transferase activity; IEA.
GO; GO:000648; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR011019; Prot_kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 17; DB 2; Length 128; 20.0%; Pred. No. 2.6; tive 0; Mismatches 8; Indels
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003873; BAD08805.1; -.
Hypothetical protein:
SEQUENCE 139 AA; 14109 MW; E281360370FB63C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 AA; 14115 MW; D30AC8C668621B0C CRC64;
                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ25437.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 AA
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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Best Local Similarity 20.0.
Best Local Similarity 20.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Q6ZKM7

Matches

ò 셤 RESULT 10
COSZEM
AC QGZEM
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DT 05-JUI
DE HYPOEL
GN Name=
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Gaps

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220 AA; 23719 MW; 1F40C6E7CDCCF3B8 CRC64;
    PRINTS; PR00232; POTXCARLCOAT.
ProDom; PD000603; Pltvir_coat; 1.
                                                                                Coat protein.
SEQUENCE 22
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MEDILNE-22560306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitils.";

Nat. Biotechnol. 21:526-531(2003).

GO; GO:0003700; E:transcription factor activity; IEA.

GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.

InterPro; IPR001647; HTH TetR.

Fram: PF00440; TetR. N; 1.

Complete proteome.

SEQUENCE 219 AA; 24066 MW; SCS9ADF39430F304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABOLINE=95278162; PubMed=7758973;

Ryu K.H., Yoon K.E., Park W.M.;

Ryu K.H., Yoon K.E., Park W.M.;

"Nucleotide sequence of coat protein gene of cymbidium mosaic
"nucleotide sequence of coat protein gene of cymbidium mosaic
"nucleotide sequence of coat protein gene of cymbidium mosaic
gene 156:303-304(1995).

-!- SIMILARIYT'S Belongs to the potexviruses coat protein family.

FIRB., YG4082, YG4082.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; F:structural molecule activity; IEA.

FIRE., PRO00052; Pltvir_coat.

FIRE., PRO00055; Pltvir_coat.
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                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948;
MEDLINE=21477403; PubMed=11572948;
Gmura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
metabolites.";
                                                                                                                                                         Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 2; Length 219;
Pred. No. 3.3;
0; Mismatches 8; Indels
01.-UUN-2003 (TrEMBLrel. 24, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative TetR-family transcriptional regulator.
OrderedLocusNames=SAV7510;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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20.0%;
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Cymbidium mosaic virus.
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Bukaryota, Vidiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
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65.4%; Score 17; DB 2; Length 220; 20.0%; Pred. No. 3.3; ive 0; Mismatches 8; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Katayose Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR005918; BAD10719.1; -.
Hypothetical protein.
SEQUENCE 256 AA; 26591 MW; 63BFCAF53D2D40EA CRC64;
                                                                                                                                                                                                                                                                     OGYTS2;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein P0419909.29.
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Matches 2; Conservative
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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
         Copyright
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OM protein - protein search, using sw model

December 29, 2004, 21:19:46; Search time 94 Seconds (without alignments) 38.163 Million cell updates/sec Run on:

US-10-046-922-34 56 score: Title: Perfect (

1 XGYWLTIWGX 10 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

2002273 segs, 358729299 residues Searched:

444336 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneedin 1980s: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

		de			SUMMAKIES		
Result No.	Score	Query Match	Length	DB	ID	Description	ion
-	54	96.4	10	5	ABP53931	Abp53931	VEGFR-3 b
~	54	96.4	10	ហ	ABP53932	Abp53932	VEGFR-3 b
٣	33	58.9	7	ហ	ABP53964	Abp53964	VEGFR-3 b
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9	32	57.1	7	m	AAY76794	Aay76794	Somatosta
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10	31	55.4		œ	ADN64476	Adn64476	HLA bindi
11	31	55.4	10	4	AAG95260	Aag95260	Human com
12	30.5	54.5	10	~	AAR14709	Aar14709	Labaditin
13	30	53.6	თ	4	AAU02369	Aau02369	HLA bindi
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12	30	53.6	10	4	AAB99759	Aab99759	Rhesus D
16	30	53.6	10	œ	ADG94728	Adg94728	Human JAM
17	30	•	10	œ	AD147102	Adi47102	Permeabil
18	30	53.6	10	00	ADP87303	Adp87303	Human cla
19	29	51.8	S	~	AAR29452	Aar29452	Endotheli
20	29	51.8	S	N	AAR69224	Aar69224	Endotheli
21	29	51.8	ß	~	AAW56531	Aaw56531	Antigenic
22	29	51.8	7	æ	ADJ25834	Adj25834	Tyrosine
23	29	51.8	80	4	ABP22594	Abp22594	HIV All m
24	29	51.8	æ	4	ABP14287	Abp14287	HIV A03 B
25	29	51.8	αο	4	ABP18686	Abp18686	HIV B62 B

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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 5

ALIGNMENTS

RESULT 1

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. /note= "any amino acid" 'note= "any amino acid" VEGFR-3 binding peptide SEQ ID NO:34. Location/Qualifiers ABP53931 standard; peptide; 10 AA. (LUDW-) LUDWIG INST CANCER RES. (LICN) LICENTIA LTD. 17-JAN-2001; 2001US-0262476P. 16-JAN-2002; 2002WO-IB000099. (first entry) Misc-difference Misc-difference WO200257299-A2 Homo sapiens. Synthetic. 25-JUL-2002. 09-JAN-2003 ABP53931; ABP5393:

Claim 12; Page 80; 149pp; English

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Kubo H;

Alitalo K, Koivunen E, WPI; 2002-691521/74.

The present invention describes an isolated peptide (I) that binds to and

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have cytostatic, hepatotropic, antiinflammatory, hypotenaive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, pancreas, colon, stomach, breast, endometrium, prostate, testicle, pancreas, colon, stomach, breast, endometrium, prostate, testicle, overy, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neconscullarisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangloms and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; heparotropic; antiinflammatory; hypotensive; antiidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-tranma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
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nhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
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liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangionas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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skin, head and neck, oesophagus, bone, marrow or blood, and diseases neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepstitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kubo
                                                                                                                                                                                                                                                                     58.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001US-0262476P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LICENTIA LTD
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                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Misc-difference 4
                                                                                                                                                                                                                                                                                                                                                                                               GYWLTIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GYWXXXW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200257299-A2
                                                                                                                                                                                                      Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP53965;
                                                                                                                                                                                                                                                              Query Match
Best Local
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ABP53965
ABP53965
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
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                                                                                                                                                             Gaps
skin, head and neck, oesophagus, bone, marrow or blood, and diseases
               neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                              ö
                                                                                                                                                             3; Indels
                                                                                                                              Length 8;
                                                                                                                              Score 33; DB 5; 1
Pred. No. 1.7e+06;
                                                                                                                  58.9%; Scor.
57.1%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "X is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "X is any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                         VEGFR-3 binding peptide SEQ ID NO:73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 147; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kubo H;
                                                                                                                                                                                                                                                                                                            ABP53968 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                             Query Match
Best Local Similarity 57.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alitalo K, Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-691521/74.
                                                                                                                                                                                                                           1 GYWXXXW 7
                                                                                                                                                                                             2 GYWLTIW 8
                                                                 present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200257299-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                           09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-2002.
                                                                                                Sequence 8
                                                                                                                                                                                                                                                                                                                                           ABP53968;
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                                                                                                                                                                                                                                                                            RESULT
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02-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                      ABP53418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hornik
                                                                                                                                                                                                                                                                     ABP53418
                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                  Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; pancreatitis; atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has one building unit containing a nitrogen atom of the peptide backbone connected to a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected via a bridging group to form a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders such as cancers, autoimmune diseases, endocrine disorders, diabeticases completed complications, gastrointestinal disorders, inflammatory
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                                                                                                              Gaps
 neck, oesophagus, bone, marrow or blood, and diseases
          neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabbetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
                                                                                                              ö
                                                                                        Length 10
                                                                                                            3; Indels
                                                                                      Score 33; DB 5; 1
Pred. No. 1.3e+02;
                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                              Somatostatin analogue peptide 3181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 11; Page 61; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gellerman
                                                                                                                                                                                                               AAY76794 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Trp-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-IL000329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00100360
98US-00203389
                                                                                      58.9%;
57.1%;
                                                                                                                                                                                                                                                        (first entry)
                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Afargan MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-136888/12.
                                                                                                                                 2 GYWLTIW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEPT-) PEPTOR LTD.
                                                                                                 Local Similarity
                                                                                                                                                      GYWXXXW 8
                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                  Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9965508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1998;
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                                                                                                                                                                                                                                                        20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumors.
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hornik V,
                                                                                                                                                                                                                                  AAY76794;
                                                                                        Query Match
                                                                                                            Matches
                                                                                                                                                                                     RESULT 6
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                   pain. It may also be used for diagnosing cancer. The backbone cyclic analogue is used for imaging the existence of metastases. Somatostatin analogues can be used for the treatment patients with hormone-secreting and hormone-dependent tumours. They reduce diarrhoea through the inhibition of vasoactive intestinal peptide (VIP) secretion and by direct effect on intestinal secretion. Somatostatin analogues selective to type 2 and 5 receptors may be used for treatment of non-insulin dependent diabetes mellitus. They are useful for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatostopin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer; antidiabetic; antinflammatory; somatostatin receptor ligand; cancer; atherosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis; pancreatitis; post-surgical pain.
atherosclerosis, restenosis and post-surgical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New backbone cyclized somatostatin analogs are e.g. useful in the treatment of atherosclerosis, autoimmune diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 3; Length 7;
Pred. No. 1.7e+06;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-terminally modified with Fmoc
(fluorenylmethoxycarbonyl) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Backbone cyclised somatostatin analogue PTR 3181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "D form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gellerman G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                        their in-vivo activities and safe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP53418 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00100360.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00203389
99WO-IL000329
                                                                                                                                                                                                                                                                                                                                                                                                                                 57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Afargan MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HORN/) HORNIK V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-681319/73.
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GYWLTIW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GYWKVCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002052315-A1.
                                                                                                                                                                                                                                                                                                                                                                    Sequence 7 AA;
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02-DEC-1998;
15-JUN-1999;
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Gaps

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Sequence 8 AA;

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(DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON
                                                                                                                                                                                                   Antigenic site of HN protein loop beta-4L23.
Example 12; Page 21; 30pp; English.
                                                                                                                                                                     AAW97529 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                        Langedijk JPM, Van Oirschot JT;
                                                                                                                                                                                                                                                           98WO-NL000390.
                                                                                                                                                                                                                                                                    97EP-00202100.
                                                                                                              57.1%;
57.1%;
                                                                                                        Ouery Match
Best Local Similarity 57.1%,
Best Local 4; Conservative
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                  WPI; 1999-120896/10.
                                                                                                                                  Φ
                                                                                                                                           1 GYWKVCW 7
                                                                                                                                  GYWLTIW
                                                                                                    Sequence 7 AA;
                                                                                                                                                                                                                             Measles virus
                                                                                                                                                                                         19-MAY-1999
                                                                                                                                                                                                                                      WO9902695-A2
                                                                                                                                                                                                                                                                    08-JUL-1997;
                                                                                                                                                                                                                                                          08-JUL-1998;
                                                                                                                                                                                                                                                21-JAN-1999
                                                                                                                                                                              AAW97529:
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The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and wulnerary activities, and can be used in gene therapy. diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of necovascularisation, e.g. liver diseases, hypertension, post-trauma, ohronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    angiogenesis, lymphangiogenesis, vascular endothelial growth factor, cytostatic, hepatotropic, antiinflammatory; hypotensive, antidiabetic; uninerary; cell surface receptor; cancer; neovascularisation; liver disease, hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.4%; Score 31; DB 5; Length 9; 57.1%; Pred. No. 1.7e+06; ive 0; Mismatches 3; Indels
                                                                             0; Indels
                           Length 8;
                        55.4%; Score 31; DB 2; Lv
100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGFR-3 binding peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Page 80; 149pp; English.
                                                                                                                                                                                                                                                                                                                         ABP53933 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kubo H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JAN-2002; 2002WO-IB000099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alitalo K, Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LICN ) LICENTIA LTD.
Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                  3 YWLTI 7
                                                                                                                                                                                    4 YWLTI 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                              ABP53933;
                                                                                                                                                                                                                                                                                                ABP53933
                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                 셤
                The present invention describes backbone cyclised somatostatin analogues

(I) that incorporates at least one building unit containing one nitrogen

atom of the peptide backbone connected to a bridging group (comprising an

anide, thioether, thioester or disullide) where at least one building an

anide, thioether, thioester or disullide) where at least one building

unit is connected via the bridging group to form a cyclic structure with

a moiety selected from the group consisting of a second building unit,

the side chain of an amino acid residue of the sequence or the N-terminal

cytostatic, antidiabetic, antiinflammatcry and analgesic activities, and

can be used as somatostatin receptor ligand. (I) are useful in the

treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-

associated complications, endocrine disorders, inflammation.

Gastrointestinal disorders, pancreatitis, post-surgical pain, and

restenosis. (I) can also be used in the diagnosis of cancer, by imaging

the existence of metastases, it being labeled with a detectable probe.

The present sequence represents a backbone cyclised somatostatin analogue
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neuraminidase (HN) protein of the paramycovitides. The specification
describes 3-D models identifying a proteinaceous substance comprising at
least one virus epitope derived from the attachment protein, which
corresponds to an antigenic site present on one of the loops of HN. The
antigenic sites can be used to produce vaccines, to detect the viruses,
and to select the immunodominant epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated proteinaceous substance - comprising at least one virus epitope derived from an attachment protein of a paramyxovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae; virus epitope; attachment protein; vaccine; immunodominant epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 5; I Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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GYWLTIW

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13-DEC-1999;
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24-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Labaditin.
                                                                 AAG95260;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel composition comprising one or more peptides or nucleic acids encoding an HLA binding peptide. The composition further comprises an HTL epitope. It also comprises a spacer molecule, a carrier, an MHC targeting sequence or a lipid. The peptides are incorporated as part of a liposome. The peptide is from an antigen are incorporated as part of a liposome. The peptide is from an antigen selected from prostate specific antigen (PSA), prostate specific membrane antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV) antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, HUW and immunodeficiency type-1 (HIV-I), human immunodeficiency type-2 (HIV-2), amtine p53 (mp53), CEA, HERZ/neu, and tyrosine kinase related protein (TKP). The composition is useful for preventing or treating viral infections or cancer, such as prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyloma acuminatum. The composition is also be used for diagnosing such diseases. This sequence represents a peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition of peptides and nucleic acids capable of binding Major Histocompatibility Complex molecules, useful for diagnosing, preventing or treating viral infections or cancer, such as prostate cancer, hepatitis B or AIDS.
                                                                                                                                                                                                       gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome; prostate specific antigen; prostate specific membrane antigen; hepatitis C virus antigen; hepatitis C virus antigen; mailgnant melanoma antigen; Bestein Barr virus; cancer; prostate cancer; AlDS; renal carcinoma; cervical carcinoma; lymphoma;
                                                                                                                                                                                            cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.4%; Score 31; DB 8; I 60.0%; Pred. No. 1.7e+06; iive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1076; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sette A;
                                                                              ADN64476 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2003; 2003WO-US031308
                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2002; 2002US-0416207P, 08-OCT-2002; 2002US-0417269P.
                                                                                                                                                               HLA binding peptide #1076.
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Southwood S,
                                                                                                                                                                                                                                                                                chondyloma acuminatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-347953/32.
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tes 3; Conserv
GYWWDTW
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                                                                                                                                                                                                                                                                                                            Jnidentified.
                                                                                                                                      01-JUL-2004
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                                                                                                          ADN64476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as lead ligands to facilitate drug design and development. The present sequence is a complementary peptide provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                        Human; complementary peptide; ligand; drug discovery; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 4; Le
Pred. No. 2.5e+02;
1; Mismatches 2;
                                                                                                                 Human complementary peptide, SEQ ID NO: 1454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclic; immunoglobulin; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 250; 646pp; English.
AAG95260 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR14709 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                   13-DEC-2000; 2000WO-GB004776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.4%;
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(first entry)
                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            candidates or pro-drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Heal JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the specification
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                                                                                                                                                                                                                                                                                                                                                                                                 (PROT-) PROTEOM LID
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GYWLTIWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVWLTVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 AA;
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The peptide is isolated from plants of the Euphorbiaceae family (see FEBS Letters 256, 1-2, 1989). It selectively inhibits the classical activation pathway of the complement system by binding to IGG. It can be used to treat autoimmune disorders e.g. rheu- matic and other inflammatory disorders, and immuno-complex-related diseases, e.g. extrinsic allergic alveolitis. It may also be used to isolate IGG from blood plasma or serum to reduce the level of IgG, or as immunoassay reagent to determine IgG levels in body fluids. See also AAR14710. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; extracellular serine protease; tumour antigen derived gene-16;
TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;
prostate cancer; HLA type.
                                                                                                                                                  New cyclic peptide(s) e.g. labaditin, having IgG binding properties used for IgG binding in mammals including humans and for treating inflammatory diseases including rheumatic and auto:immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumor antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                        Score 30.5; DB 2; Length 10;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'brien TJ, Underwood LJ, Shigemasa K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; Page 55; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA binding TADG-16 peptide #145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU02369 standard; peptide; 9 AA.
                                                                                                                                                                                                          Claim 11; Page 12; 15pp; English
             90US-00512796
                                        90US-00512796
                                                                                                                                                                                                                                                                                                                                                                                                        54.5%;
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                                                                  (UYUT-) RIJKSUNIV UTRECHT
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
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                                                                                                                        WPI; 1991-339755/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYWLTIWG
                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 AA;
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             23-APR-1990;
                                        23-APR-1990;
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                                                                                             Labadie RP;
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AAU02225-AAU02384 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA A24, HLA B27, HLA B2702, and HLA B4031, Tumour antigen derived gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular serine protease. TADG-16 is expressed in normal ovaries and testes and in certain ovarian carcinomas. TADG-16 contains the conserved catalytic triad, His-Asp-Ser, and a signal secretion sequence characteristic of the serine protease family. An antisense oligonucleotide having a complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 are useful for the diagnosis of cancer. TADG-16 protein or its fragments are useful for vaccinating an individual against TADG-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU02225-AAU02384 represent TADG-16 peptides which are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA A24, HLA B7, HLA B8, HLA B2702, and HLA B4031. Thmour antigen derived gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular serine protease. TADG-16 is expressed in normal ovaries and testes and in certain ovarian carcinomas. TADG-16 contains the conserved catalytic triad, His-App-Ser, and a signal secretion sequence characteristic of the serine protease family. An antisense oligonucleotide having a complementary sequence to the TADG-16 nucleic acid is useful for treating various cancers, including ovarian, breast, lung, colon and prostate. The TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16 are useful for the diagnosis of cancer. TADG-16 protein or its fragments are useful for vaccinating an individual against TADG-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, extracellular serine protease, tumour antigen derived gene-16; TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer; prostate cancer; HLA type.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New tumor antigen-derived gene-16 protein, useful for diagnosis and treatment of ovarian, breast, lung, colon and prostate cancer.
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                                                                                                                                                                                                                                                                                                                                 53.6%; Score 30; DB 4; Length 9; 66.7%; Pred. No. 1.7e+06; ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU02282 standard; peptide; 9 AA.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     4 WLTIWG
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                                                                                                                                                                                                                                                                                          Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                         Gaps
                                                                                                                                                                                       D antibody binding peptide; Rhesus D; RhD; identification;
                                                                                                                                                                                              anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; idiopathic thrombocytopaenic purpura; immunoglobulin.
                                         ö
                         Length 9;
                        Score 30; DB 4; I
Pred. No. 1.7e+06;
L; Mismatches 1;
                                                                                                                                                                     Rhesus D antibody binding peptide SEQ ID NO:4.
                                                                                                                    AAB99759 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                     Fisch I;
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1, Page 12; 19pp; English.
                                                                                                                                                                                                                                                                                   99EP-00122858
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                        53.6%;
                                                                                                                                                      (first entry)
                                         Conservative
                                                                                                                                                                                                                                                                                                                   (ZLBB-) ZLB BIOPLASMA AG
                                                                                                                                                                                                                                                                                                                                     Hofmann A,
              Query Match
Best Local Similarity
4, Conserv?
                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-383568/41.
                                                                    |:| ||
WVTGWG 6
                                                         WLTIWG 9
        Sequence 9 AA;
                                                                                                                                                                                                                                                 EP1106625-A1.
                                                                                                                                                                                                                                                                                   17-NOV-1999;
                                                                                                                                                                                                                                                                                                    17-NOV-1999;
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                     21-SEP-2001
                                                                                                                                                                                                                                                                  13-JUN-2001.
                                                                                                                                                                                                                                                                                                                                     Miescher S,
                                                                                                                                     AAB99759;
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Score 30; DB 4; Length 10;
Pred. No. 3.5e+02;
0; Mismatches 3; Indels
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Job time : 97.3333 secs
    Similarity 57.1%;
4; Conservative (
    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                  2 GYWLTIW 8
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Sequence 10 AA;

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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                               CITY: Washington STATE: D.C.
Sequence 34, Appl
Sequence 348, Appl
Sequence 13, Appl
Sequence 1649, Ap
Sequence 12, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 1897, Ap
Sequence 1587, Ap
Sequence 2474, Ap
Sequence 2474, Appl
Sequence 2474, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 28, Appl
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4, Appli
5, Appli
6, Appli
1500, Ap
5, Appli
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9, Appli
                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                          December 29, 2004, 21:20:27 ; Search time 23.6667 Seconds (without alignments) 28.022 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Sequence S
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Sequence
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Sequence
Sequence
                                                                                                                                                                                                                                                               Issued Patents AA:*

1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                      5-08-415-099A-4
5-08-467-472C-5
5-08-467-472C-6
5-09-082-279B-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-834-784-1500
US-08-632-444B-9
                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-384-061-5
-09-384-061-6
                                                                                                                                                              478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                             US-10-046-922-34
56
                                                                                                                 1 XGYWLTIWGX 10
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                 Copyright
                                                                                                                                                                                                  seq length: 0
seq length: 10
                                                                                                                                                                                                                                                                                                                                                                                            Query
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                                                                                                Title:
Perfect score:
                                                                                                                                    Scoring table:
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                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                                                                              Searched:
                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                 Database
                                                             Run on:
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Result No.

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Sequence
Sequence
Sequence
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Sequence
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Sequence
Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-09-069-827A-94
is Sequence 94, Application US/09069827A
j Patent No. 6617114
j GENERAL INFORMATION:
KAY, Baian K
KAY, Baian K
FRELINGER, Jeffrey A
HYDE-DERUYSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER FEALURE FURDED disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION TOWNER: US/09/069,827A
FILING DATE: 31-Apr-1998
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATE:
APPLICATION DATE: 31-Apr-1998
APPLICATION NUMBER: US 09/050,359
FILING DATE: 31-APR-1997
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-OCT-1997
APPLICATION NUMBER: US 08/740,671
FILING DATE: 31-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
US-09-350-641C-1655
US-09-852-870A-5
US-08-982-870A-5
US-08-982-870A-6
US-08-632-444B-10
US-09-620-091-41
US-09-620-091-41
US-09-191-571-21
US-09-155-106-1
US-09-155-106-1
US-09-125-641-2
US-09-126-641-2
US-09-126-641-2
US-08-104-144-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: FOWLKES=4C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7 amino acide
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Gaps

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Sequence 13, Application US/08735253
Patent No. 5942491
GENERAL INFORMATION: Abelian Robert S.
TITLE OF INVENTION: Methods and Compositions for Treating TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.8%; Score 29; DB 2; Length 10; Best Local Similarity 42.9%; Pred. No. 1.6e+02; Matches 3; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB 2; Length 10;
Pred. No. 1.6e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd. STREET: 180 N. Stetson CITY: Chicago CITY: Chicago STATE: Illinois COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOGTWARE: Patentiun Release #1.0, Version #1.30
SOGTWARE: PATENTION NUMBER: US/08/735,253
FILING DATE:
TLASSIFICATION NUMBER: US/08/735,253
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5942491Hrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: MIC3302P0010US
              ATTORNEY/AGENT INFORMATION:
NAME: No. 5942491thrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: MIC3302P0010US
TELECOMMUNICATION INFORMATION:
TELEFAK: (3120 616-5460
TYPE: AMINO ACID NO: 8:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acid acids
TYPE: amino acid acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13:
                                                                                                                                                                                                                                                                                                                                                                                                          51.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-735-253-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YWLTIWG 9
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1 FWRFLWG 7
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  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Stete, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Epimmue Inc.
TITLE OF INVENTION: Emmue Response and Methods of Using the Same
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 3963-2002.01
CURRENT APPLICATION NUMBER: US 60/085,751
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR PRILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 9
                                                                                                Gaps
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Patent No. 5942491;
GENERAL INFORMATION:
APPLICANT: Root-Bernstein, Robert S.
TITLE OF INVENTION: Methods and Compositions for Treating TITLE OF INVENTION: Archritis
NUMBER OF SEQUENCES: 19;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson
STRY: Chicago
STRY: Chicago
STRY: US.A.
                                            51.8%; Score 29; DB 4; Length 7; 57.1%; Pred. No. 3.8e+05; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.8%; Score 29; DB 4; Length 9; 80.0%; Pred. No. 3.8e+05; ive 1; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,253
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)
US-09-311-784A-348
                                                                                                                                                                                                                                                                                    US-09-311-784A-348
; Sequence 348, Application US/09311784A
; Patent No. 6534482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0
اتام 4، Conservative
                                                                                             Conservative
                   Query Match
Best Local Similarity
                                                                                                                                          3 YWLTIWG 9
                                                                                                                                                                                        1 YWWPDWG 7
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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4 LTVWG 8
US-09-069-827A-94
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Gaps

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NAME: FEITAIO, GREGOTY D.
REGISTRATION UNUBER: 36,134
REFRENCE/DOCKET NUMBER: 4-90(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6923
TELEPHONE: (908) 522-6923
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.0
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 214320
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO FRAGMENT TYPE: internal US-09-125-641-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 amino acida
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-191-571-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYBEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT APPLICATION NUMBER: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1649
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Stadler, Beda
TITLE OF INVENTION: Peptide Immunogens For Vaccination
TITLE OF INVENTION: Peptide Immunogens For Vaccination
TITLE OF INVENTION: Against and Treatment of Allergy
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 661029/artis Corporation
STRRET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07901
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 28; DB 3; Length 8; 50.0%; Pred. No. 3.8e+05;
                                                                           RESULT 5
US-09-315-304B-1649
Sequence 1649, Application US/09315304B
PERTAL NO. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-125-641-3
; Sequence 3, Application US/09125641
Patent No. 6610297
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0
Best Local Similarity 50.0
Matches 3; Conservative
   1 FWRFLWG 7
                                                                                                                                                                                                                                                                                                                    APPLICANT: Merutka,
APPLICANT: Anwer, M
APPLICANT: Lambert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WLTIWG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WNSLWG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: HIV-1
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   엄
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Patent No. 5521156

GENERAL INFORMATION:
APPLICANT: Owen, Thomas J.
APPLICANT: Buck, Stephen H
APPLICANT: Marbeson, Scott L
TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS: AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,571
FILING DATE: 03-FEB-1994
CLASSIFICATION: 514
ATTONEX/AGENT INFORMATION:
NAME: BOUNTERNING WIlliam R
REGISTRATION NUMBER: 35,796
REFRENCE/DOCKET NUMBER: 35,796
TELEPROMINICATION INFORMATION:
TELEPROMINICATION INFORMATION:
TELEPROMINICATION INFORMATION:
TELEPRAK: 513-948-6566
TELEPRAK: 513-948-7961 or 4681
4-900-9862/A/NFI/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States
ZIP: 45215-6300
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 7..8
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US-09-082-279B-1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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Patent No. 6241965

Patent No. 6241965

GENERAL INFORMATION:

APPLICANT: McBride, William
APPLICANT: Conceptual Macker Drive, Suite 3000
CITY: Chicago
                                                                                                                                                      APPLICANT: Merrell Dow Pharmaceuticals Inc.
TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Marion Merrell Dow Inc.
ADDRESSE: Marion Merrell Dow Inc.
CITY: Cincinnati
                                                                                                                                                                                                                                                                                                                        COUNTRY: UGA

ZIP: 45215-6300

COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00296
FILING DATE:
CLASSIFICATION:
NAMME: BOUGREAUX, William R
REGISTRATION NUMBER: 35,796
REFERENCE/DOCKET NUMBER: M01718A WO
TELECOMMUNICATION INFORMATION:
TELEFHONE: 513-948-7961 or 4681
TELEFA: S13-948-7961 or 4681
INFORMATION FOR SEQ ID NO: 12:
SECULENCE CHARACTERISTICS:
LEBNGTH: 6 amino acids
                                                                                                         Sequence 12, Application PC/TUS9500296; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: peptide
PCT-US95-00296-12
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Best Local Similarity
Matches 5; Conserva
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YWLTIWG 9
                                    1 YWLR-WG 6
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COUNTRY:
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NAME/KEY: Modified-site
LOCATION: 1..4
COTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
OTHER INFORMATION: is L-4-chlorophenylalanine; the Trp is in the
OTHER INFORMATION: D conformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The carboxyl group of the C-terminal
; OTHER INFORMATION: Thr is reduced to an alcohol;
US-08-586-670A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..2
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "Phe is in the D conformation and is
OTHER INFORMATION: linked to DTPA;
FRATURE:
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i Sequence 1495, Application US/09082279B

j Patent No. 62587B2

j GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: PHARID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 787-043
CURRENT APPLICANTON: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 787-043
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SEQ ID NO 1495
LEAGTH: BARGED FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/586,670A
FILING DATE: 22-APR-1996
CLASSIFICATION: 42-APR-1996
CLASSIFICATION: 42-APR-1996
TLASSIFICATION: WOMER: 35.303
REGISTRATION NUMBER: 92,385-DD
TELERPONE: 312-715-1000
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Gaps

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APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Guthrie, K.
APPLICANT: Menutka, G.
APPLICANT: Menutka, G.
APPLICANT: Amwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTYON: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTY APPLICATION NUMBER: US/09/315,304B
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT APPLICATION NUMBER: 09/06.20
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: PRAESEQ for Windows Version 3.0
SEQ ID NO 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47, Application US/09350325
| Sequence 47, Application US/09350325
| Patent No. 624020
| GENERAL INFORMATION:
| APPLICANT: Ding, S. |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF |
| TITLE OF INVENTION: THERAPEUTIC REAGENTS |
| FILE REPERENCE: 787-2062 |
| CURRENT FILING DATE: 1999-07-09 |
| NUMBER OF SEQ ID NOS: 49 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| LENGTH: 10 |
| LENGTH: 10 |
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48.2%; Score 27; DB 3; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels
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  1; Indels
  2; Mismatches
                                                                                                                                                                                  Sequence 1587, Application US/09315304B Patent No. 6348568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
  3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
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1 GGWASLW
                                           4 WLTIWG
                                                                  1 WDSLWG
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  Matches
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APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYBEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYBEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: HYBRID POLYBEPTIDES
FILE REFERENCE: 7872-067
CURRENT FAPLICATION NUMBER: 08/09/35,304
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SEQ ID NOS: 1757
SEQ ID NO 1650
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                                                            1; Indels
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                     Length 8;
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Merutka, General APPLICANT: Merutka, General APPLICANT: Anwer, Mohmed APPLICANT: Lambert, Dennis TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED TITLE OF INVENTION: PRARMACOKINETIC PROPERTIES FILE REPRENCE: 7972-043 CURRENT APPLICATION NUMBER: US/09/834, 784 CURRENT FILING DATE: 2001-04-13 PRIOR APPLICATION NUMBER: 09/082, 279 PRIOR FILING DATE: 1998-05-20 NUMBER OF SEQ ID NOS: 1515 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1495 LENGTH: 8
                   Score 27; DB 3; 1 Pred. No. 3.8e+05;
        48.2%; Scc...
50.0%; Pred. No. s.c...
2; Mismatches
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                                                                                                                                                                                             RESULT 11
US-09-834-784-1495
; Sequence 1495, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Metutka, Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1650, Application US/09350641C Patent No. 65656906 GENERAL INFORMATION: APPLICANT: Barney, S.
Query Match
Best Local Similarity 50.v
13. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Conservative
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Merutka, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::||
WDSLWG 6
                                                                                                                            | ::||
1 WDSLWG 6
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                                                                                                   WLTIWG 9
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US-09-350-641C-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: HIV-1
US-09-350-641C-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-834-784-1495
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Gaps

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                               Sequence 1587, Application US/09350641C

Batent No. 6656906

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, M.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: HYBRE: US/09/350,641C

CURRENT APPLICATION NUMBER: 09/092,279

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 1757

SEQ ID NO 1587

LENGTH: 10

LENGTH: 10
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Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Core polypeptide
US-09-350-641C-1587
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1 GGWASLW 7
RESULT 15
US-09-350-641C-1587
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Search completed: December 29, 2004, 21:36:44 Job time: 24.6667 secs

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Sequence 348, Sequence 348, Sequence 348,

Sequence 180, App Sequence 181, App Sequence 792, App Sequence 837, App Sequence 837, App Sequence 837, App Sequence 1271, Ap Sequence 92, Appl Sequence 92, Appl Sequence 7, Appli Sequence 70, Appl Sequence 70, Appl Sequence 69, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 14, Appl Sequence 14, Appl Sequence 150, Appl Sequence 150, Appl Sequence 160, Appl Sequence 160, Appl Sequence 180, Appl Sequence 180, Appl

1 US-10-371-069-348 1 US-10-371-645-348 2 US-10-182-252A-180 2 US-10-182-252A-181 2 US-10-182-252A-181 2 US-10-182-252A-793 3 US-10-182-252A-793 5 US-10-182-252A-837 5 US-10-182-252A-837 5 US-10-182-252A-837 6 US-10-182-252A-837 7 US-10-182-252A-837 8 US-10-132-252A-837 1 US-10-133-210-70 4 US-10-133-210-70 4 US-10-133-210-70 4 US-10-133-210-70 4 US-10-20-708-353 4 US-10-20-708-353 4 US-10-20-708-353 5 US-10-20-708-353 6 US-10-20-708-353 7 US-10-20-708-353 8 US-10-20-708-353 9 US-10-20-708-363 9 US-10-23-656-11 9 US-10-23-656-11 9 US-10-23-656-14 9 US-10-23-656-34 9 US-10-23-656-34 9 US-10-23-656-34 9 US-10-23-656-34 9 US-10-23-656-34 9 US-10-23-656-34 9 US-10-23-656-34

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US-10-046-922-34
 December 29, 2004, 21:36:53; Search time 82 Seconds (without alignments) 43.869 Million cell updates/sec
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(gan2_6/ptodata/2/pubpaa/US07_NEW_PUB. DED: *

(gan2_6/ptodata/2/pubpaa/US06_PUBCOMB. DED: *)

(gan2_6/ptodata/2/pubpaa/US07_NEW_PUB. DED: *)

(gan2_6/ptodata/2/pubpaa/US07_NEW_PUB. DED: *)

(gan2_6/ptodata/2/pubpaa/US08_PUBCOMB. DED: *)

(gan2_6/ptodata/2/pubpaa/US08_PUBCOMB. DED: *)

(gan2_6/ptodata/2/pubpaa/US08_PUBCOMB. DED: *)

(gan2_6/ptodata/2/pubpaa/US08_PUBCOMB. DED: *)

(gan2_6/ptodata/2/pubpaa/US09_REW_PUB. DED: *)

(gan2_6/ptodata/2/pubpaa/US09_NEW_PUB. DED: *)

(gan2_6/ptodata/2/pubpaa/US09_NEW_PUB. DED: *)

(gan2_6/ptodata/2/pubpaa/US09_NEW_PUB. DED: *)

(gan2_6/ptodata/2/pubpaa/US10B_PUBCOMB. DED: *)
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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56
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                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 10
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Match
                                                                                                                                                                   Title:
Perfect score:
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ALIGNMENTS

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Gaps
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US-10-U46-922-34

Sequence 34, Application US/10046922

Publication No. US20020164667A1

GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: WIGER:
TITLE OF INVENTION: VOGER:
CURRENT PAPLICATION NUMBER: US/10/046,922

CURRENT PAPLICANTON: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SEQ ID NO 34

LENGTH: 10

MAME/KEY: SITE

LOCATION: (1): (1)

OTHER INFORMATION: X is any amino acid
US-10-046-922-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.4%; Score 54; DB 13; Length 10; 100.0%; Pred. No. 0.22; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 8; Conservative
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GYWLTIWG 9 GYWLTIWG 9

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Sequence 35, Appl Sequence 67, Appl Sequence 68, Appl Sequence 73, Appl Sequence 1454, Appl Sequence 1157, Appl Sequence 1157, Appl Sequence 1158, Appl

US-10-046-922-34 US-10-046-922-35 US-10-046-922-67 US-10-046-922-68 US-10-046-922-73 US-10-046-922-36 US-10-046-922-36 US-10-046-922-36 US-10-462-452-707 US-09-572-404B-1454 US-09-894-018-154 US-09-894-018-154 US-10-133-210-8

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Sequence 34, App.

Description

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APPLICANT: Alitalo, Kari
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VBGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 2896/737084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 73
LENGTH: 10
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Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILLS REFRESENCE: 28967/37084A
CURRENT APPLICATION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILLS REFRESENCE: 28967/37084A
CURRENT PILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 13; Length Lughed. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                              h Similarity 57.1%; Pred. No. 1.5e+06; 4; Conservative 0; Mismatches 3; Indels
                                                                                                        TYPE: PRT
ORGANISM: peptide
FEATURE:
NAME/KEY: SITE
LOCATION: (4)..(6)
OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
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OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
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; OTHER INFORMATION: X is any amino acid
US-10-046-922-73
                                                                                                                                                                                                                                                            LOCATION: (8)..(8)
OTHER INFORMATION: X is any amino acid
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CURRENT FILING DATE: 2002-01-1
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.0
SEQ ID NO 68
LENGTH: 8
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Best Local Similarity 57.1%;
Matches 4; Conservative
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FEATURE:
NAME/KEY: SITE
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Publication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Kolovunen, Erki

APPLICANT: Kolovunen, Erki

APPLICANT: Kolovunen, Erki

APPLICANT: Robo, Hajime

TITLE OF INVENTION: VEGRR-3 INHIBITOR MATERIALS AND METHODS

TITLE OF INVENTION: UNGER.3

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

SEQ ID NO 67

LENGTH: 7
                                   Sequence 35, Application US/10046922

Publication No US20020164667A1

GENERAL INPOWATION:

APPLICANT: Roivunen, Erki

APPLICANT: Roivunen, Erki

APPLICANT: Roivunen, Erki

APPLICANT: Roivunen, Erki

TITLE OF INVENTION: VEGR-3 INHIBITOR MATERIALS AND METHODS

FILE REFERENCE: 28967/37084A

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SEQ ID NO 35

LENGTH: 10
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Sequence 68, Application US/10046922
Publication No. US20020164667A1
GENERAL INCRMATION,
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
                                                                                                                                                                                                                                                                                                                                                                                                                                   96.4%; Score 54; DB 13; Length 10; 100.0%; Pred. No. 0.22; tive 0; Mismatches 0; Indels
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; OTHER INFORMATION: X at position 4-6 is any amino acid US-10-046-922-67
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: isolated peptide US-10-046-922-35
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 96.4
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches 4; Conserv
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ORGANISM: peptide
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                          US-10-046-922-35
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Sequence 708, Application US/1032266
Fublication No. US20040115135A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTI
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TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
TITLE OF INVENTION: Therapeutic Compounds
FILE REFERENCE: 02-03US
CURRENT APPLICATION WUMBER: 104/601,953
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR FILING DATE: 2002-66-28
NUMBER OF SEQ ID NOS: 900
SOFTWARE: Patentin version 3.2
SEQ ID NO 912
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Pred. No. 5.9e+02;
1; Mismatches 2; Indele
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         2; Indels
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Pred. No. 5.9e+02;
         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                        Sequence 812, Application US/10601953
Publication No. US20040077540Al
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.6%;
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Best Local Similarity 50.0
Matches 3; Conservative
         3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.6
Best Local Similarity 50.0
Matches 3; Conservative
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US-09-894-018-154
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         Matches
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US-09-572-404B-1454
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Sequence 1454, Application US/09572404B

Sequence 1454, Application US/09572404B

Fublication No. US2030078374A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REPERRINCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 1454
                                                                                                                                                                                                                                                                                                                     Gaps
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| Publication No. US20040037809A1
| GENERAL INFORMATION:
| APPLICANT Ouay, Steven
| APPLICANT Quay, Steven
| APPLICANT Gupta, Malini
| TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
| FILE REFERENCE: 02-02US
| CURRENT APPLICATION NUMBER: US/10/462,452
| CURRENT FILING DATE: 2003-06-16
| PRIOR APPLICATION NUMBER: 60/393,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.6%; Score 30; DB 15; Length 10; 50.0%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.4%; Score 31; DB 10; Length 10; 62.5%; Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                    Score 31; DB 13;
Pred. No. 1.5e+06;
0; Mismatches 3;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 707
LENGTH: 10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
                                                                                                                                                                                                                                                        55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.5
These 5; Conservative
                                                                                                                                                                                                                                                                                                                     4; Conservative
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ORGANISM: Homo sapiens
US-10-462-452-707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo Sapiens
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      GYWWDTW 8
                                                                                                                                                                                                                                                                                                                                                                            GYWLTIW
                                                                                                                             ; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-10-462-452-707
                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                  Matches
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Sequence 348, Application US/10371525

Publication No. US20030203869A1

GENERAL INFORMATION:

APPLICANT: Hires, John D.

APPLICANT: Hires, John D.

APPLICANT: Hires, John D.

APPLICANT: Livingston, Gary G.

APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert W.

APPLICANT: Chesnut, Robert W.

APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Immune Response and Methods of Using the Same FILE REFERENCE: 39963-20022.01

CURRENT APPLICATION NUMBER: US 09/311,784

FRIOR APPLICATION NUMBER: US 09/311,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Chesnut, Robert W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Immune Response and Methods of Using the Same FILE REFERENCE: 39963-20022.10
CURRENT APPLICATION NUMBER: US 100/078, 904
FILE REPEATON TOWER: US 09/078, 904
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.8%; Score 29; DB 14; Length 9; 80.0%; Pred. No. 1.5e+06; ive 1; Mismatches 0; Indels
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80.0%; Pred. No. 1.5e+06;
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US-10-371-069-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 348, Application US/10371069
Publication No. US20030216342A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity
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Matches 4; Conserv
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; Sequence 8, Application US/20030103964A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofeky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; TITLE OF INVENTION: COMPOSITIONS
; CURRENT APPLICANTION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARES PATENTION UP. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 1.5e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29; DB 9; Length 9;
Pred. No. 1.5e+06;
1; Mismatches 0; Indels
                                                         APPLICANT: EPINMUNE, INC.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Livingston, Brian
APPLICANT: Baker, Denisw
APPLICANT: Baker, Denisw
APPLICANT: Brown, David
APPLICANT: Brown, David
APPLICANT: Brown, Mark
APPLICANT: Brown, Mark
APPLICANT: Newman, Mark
APPLICANT: Newman, Mark
APPLICANT: Nowman, MINIGENES AND EPFTIDES THERESY
FILE REFERENCE: 3996-2003.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR SPRING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 154
LENGTH: 9
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80.0%;
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80.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Transgenic mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
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4 LTVWG 8
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LENGTH: 9
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ઠ g Matches

RESULT 13

Gaps

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                                   0; Gaps
                                                                                                                                                                                                                                                                             Query Match 51.8%; Score 29; DB 14; Length 9; Best Local Similarity 80.0%; Pred. No. 1.5e+06; Matches 4; Conservative 1; Mismatches 0; Indels
0; Indels
                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence CEATURE: OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032) US-10-371-645-348
1; Mismatches
4; Conservative
                    ||:||
4 LTVWG 8
             5 LTIWG 9
Matches
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Search completed: December 29, 2004, 22:01:39 Job time : 83 secs

5 LTIWG 9 ||:|| 4 LTVWG 8

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 29, 2004, 21:30:17 ; Search time 19 Seconds (without alignments) 50.640 Million cell updates/sec Run on:

US-10-046-922-34 56 1 XGYWLTIWGX 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

1102 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

adipokinetic hormo	T-cell receptor be	T-cell receptor be	sperm-activating p	hypotrehalosemic h	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic	hypertrehalosemic/	gonadotropin-relea	Ig heavy chain DJ	T-cell receptor be	aldehyde ferredoxi
A24244	PT0634	PT0562	A60522	B33995	808997	A60421	808998	A26381	JC1416	809138	A31571	A49187	PH1344	PH0923	A40753
0	~	7	7	~	7	~	~	~	~	0	7	~	7	~	7
0	0	σ	σ	10	10	10	10	10	10	10	10	10	10	20	10
30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4
17	17	17	17	17	17	17	17	17	17	17	17	17	17	17	17
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 S71868
glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment) N:Alternate names: glutathione S-transferase class mu 4
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: S71868
R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J. 317, 879-884, 1996
A, Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray
A; Reference number: S71864; MUID: 96332484; PMID: 8760377
A; Accession: S71868
A;Molecule type: protein
A;Residues: 1-10 <rou></rou>
A;Cross-references: UNIPROT:Q7M3E8
C; Comment: At least five species-independent classes of cytosolic glutathion transferases
s mitochondrial form are known.
C;Complex: dimer
C; Function:
A, Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a v
A; Pathway: detoxification; xenobiotics metabolism
A; Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism a
es of damage
C;Superfamily: glutathione transferase

C; Keywords: dimer; transferase

Gaps ô Query Match
42.9%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels

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4 GYW 6 2 GYW 4 g ઠ

RESULT 2

Process
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: Pr0586; Pr0592
A;Freeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: Pr0509; MUID:91277601; PMID:1711558
A;Refatus: translation not shown
A;Molecule: type: mRNA
A;Molecule: T-7 <FEE>
A;Residues: 1-7 <FEE>
A;Residues: 1-7 <FEE>
A;Residues: 1-7 <FEE>
A;Residues: T-cell receptor

a

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Gaps ö

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C;Accession: Pr0289
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jc
A;Reference number: Pr0222; MUID:91108337; PMID:1899102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P19987
CCOmment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile acts
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Wodified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 0.7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: J50315
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic IA;Reference number: J50315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain CDR3 region (clone 1-118A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10;
                                                                                                                                                                                                                                                                                                                                           Score 19; DB 2; Length 9; Pred. No. 2.8e+05; 1; Mismatches 3; Indels
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A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0324
A;Molecule type: DNA
A;Residues: 1-9 ~XAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
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32.1%; Score 18; DB 2; L
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 4;
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A,Residues: 1-10 < YAM>
A,Experimental source: B lymphocyte
C,Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 42.9%;
Matches 3; Conservative
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Best Local Similarity
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GYGESYW 9
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4 WISMGG 9
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, and of the circular muscle of the gastro-intestinal junction.
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J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gut pentapeptide - Japanese eel C; Species: Anguilla japonica (Japanese eel) C; Species: Anguilla japonica (Japanese eel) C; Species: Anguilla japonica (Japanese eel) C; Accession: J-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995 C; Accession: J-Mar-1992 #sequence_revision 7: Kubeaka, T.; Kubota, I.; Muneoka, Y.; Ando, M. Biochem. Bio
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Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)

Ig heavy chain CRD3 region (man)

C;Species: Homo sapiens (man)

C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0324
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                                                                                                           0; Indels
                   Length 7;
    Score 22; DB 2; 1
Pred. No. 2.8e+05;
1; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-10 <MAC>
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    39.3%;
Similarity 75.0%;
3; Conservative
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Matches 2; Conservative
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Best Local Similarity
Matches 3; Conserv
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SIWG 6
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Best Local S:
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C;Accession: A61068
R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992
A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, prin A;Reference number: A61068; MUID:92262851; PMID:1585017
                                                                                                                                                                                                                         J. Exp. Med. 174, 115-124, 1991
A;Tible: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Accession: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0629
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH
A;Accession: PT0528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: P70637
S;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: P70509; MUID:91277601; PMID:1711558
                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
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C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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A;Rebidues: 1-6 < SCH>
A;Cross-references: UNIPROT:P41491
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
                                                                                     T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor beta chain V-D-J region (111-1K) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: adult thymus, strain BALB/c, clone 100-4AB C; Keywords: T-cell receptor
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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WG
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Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
Affille: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-1 A;Reference number: A33932; MUID:892823; PMID:2499887
A;Accession: F33932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q99NG4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924Q1; UNIPPROT:Q924Q1; UNIPPROT:Q9DCD9; UNIPROT:Q9LR0; UNIPROT:Q9LR0; GB:M27106
C;Keywords: immunoglobulin
                     R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0230
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-10 < YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: O2-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and A;Reference number: A53284; MUID:91342695; PMID:1678859
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar_1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
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A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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Pred. No. 4.2e+03;
2; Mismatches 0;
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
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A; Residues: 1-10 < BAC>
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3 ITIFG 7
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Accession: PT0230
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PT0642
T-cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)
C;Species: Wus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0642
B. Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0642
A;Status: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Residues: 1-7 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                               T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0628
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
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F;6/Modified site: amidated carboxyl end (Gly) #status experimental
                                               Query Match 30.4%; Score 17; DB 2; Length 6; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.4%; Score 17; DB 2; Length 7; 100.0%; Pred. No. 2.8e+05; Live 0; Mismatches 0; Indels
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A;Molecule type: mRNA
A;Residues: 1-7 <FEEA
A;Experimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
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Best Local Similarity 100.0
Matches 2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
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Search completed: December 29, 2004, 21:42:54 Job time : 20 secs

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Chamaeleo melleri (Meller's chameleon).
Mitochondrion.
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
NCBI_TaxID=179915;
                                                                                                                                                                                                                                                                 NCBI TaxID=3996;
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                                                                                                                                                                                                               Labaditin.
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                                                                                                                                                                                                                                                                                  SEQUENCE
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Q8SHF6;
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Q8shn1 bradypodion
Q6j197 neisseria g
Aas16521 neisseria
Q85db0 lepilemur s
Q85db8 lepilemur s
Q95db8 lepilemur e
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Q8shf6 chamaeleo m
Q70y57 fuerstia af
Cad45547 fuerstia
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chamaeleo
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                                               December 29, 2004, 21:27:57 ; Search time 100 Seconds (without alignments) 57.537 Million cell updates/sec
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5.1.6
Compugen Ltd.
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GenCore version (c) 1993 - 2004
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QOSSIFE
QOOSTE
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CAD45547
CAD45547
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Maximum Match 100%
Listing first 45 summaries
                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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Match Length DB
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Malpighiales, Euphorbiaceae, Crotonoideae, Jatropheae,
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Q8she7
Q8shf3
Q8shf9
Q8shh1
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Q8shh3
Q8shi3
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Q8shi5
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Pred. No. 3.1e+02;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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      Q8SHF3
Q8SHF9
Q8SHG8
Q8SHH1
Q8SHH1
Q8SHH7
Q8SH13
Q8SH13
Q8SH19
Q8SH19
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                                                                                                                                                                                 Jatropha multifida (Physic nut)
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nes 5, Conservative
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 2 GYWLTIWG 9
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GVW-TVWG 8
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Chloroplast.

Bukaryock; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.

NCBL_TaxID=204226;
                                                                                                                                                                                                  Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.; "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae) based on three plastid DNA regions."; Mol. Phylogenet. Evol. 31:277-299(2004).

EMBL; AJS05427; CAD45547.1; Chloroplast; Ribosomal protein.
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Rouimi P., Anglade P., Debrauwer L., Tulliez J.;
"Characterization of pig liver glutathione S-transferases using HPLC-electrospray-ionization mass spectrometry.";
Blochem. J. 317:879-884 (1996).
PIR, ST1868; S71868.
GO, GO.0004364; Figlutathione transferase activity; IEA.
NON_TER
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glutathione transferase (EC 2.5.1.18) class mu 4 (Fragment).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                8 AA; 916 MW; DABEAB58637041B5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence v
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Cytochrome c oxidase subunit I (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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les 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                   FROM N.A.
                   uerstia africana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=9825;
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Q7M3E8;
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Matches
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DDT TO DD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.; Mylogeny and evolution of basils and allies (Ocimeae, Labiatae) based on three plastid DNA regions "; Mol. Phylogenet. Evol. 31:277-299(2004). EMBL; AJ505427; CAD45547.1; CAD45547.1; GO; GO:0003735; F:structural constituent of ribosome; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                 Townsend T., Larson A.; "Northern genomic evolution in the "Molecular phylogenetics and mitochondrial genomic evolution in the Chamaeleonidae (Reptilia, Squamata)."; Mol. Phylogenet. Evol. 23:22-36(2002).
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Pred. No. 1.8e+06;
                                                                                                                                                                                                    5E218E2733772727 CRC64;
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14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Ribosomal protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Ribosomal protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 2; I
Pred. No. 1.1e+03;
1; Mismatches 1;
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                   SEQUENCE FROM N.A.
MEDLINE=22169767; PubMed=12182400;
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10 AA; 1276 MW;
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les 3; Conservative
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2 WLLLW 6
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NON TER
SEQUENCE
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CAD45547;
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Best Local S
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CAD45547
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PubMed=15084227;
                                                        Nuol (Fragment).
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Q85DB0
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Snyder L.A., Davies J.K., Saunders N.J.;
"Microarray genomotyping of key experimental strains of Neisseria
gonorrhoeae reveals gene complement diversity and five new neisserial
genes associated with Minimal Mobile Elements.";
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                                                                                                             Townsend T., Larson A.; "More and mitochondrial genomic evolution in the "Molecular phylogenetics Squamats)."; Mol. Phylogenet. Evol. 23:22-36(2002).
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Neisseriaceae, Neisseria.
NCBI_TaxID=485;
 Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 2; Length 10;
Pred. No. 3.1e+03;
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Pred. No. 3.1e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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Snyder L.A.S., Davies J.K., Saunders N.J.;
Submitted (EEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY386266; AAS16521.1; -
                                                                                                                                                                                                                   Townsend T.M., Larson A.L.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, A448730; AAL90472.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                      NON TER 10 10 SEQUENCE 10 AA; 1327 MW; 5E2180C7336415B7 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                        [1]
SEQUENCE FROM N.A.
MEDLINE=22169767; PubMed=12182400;
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                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
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SEQUENCE FROM N.A.
Townsend T.M., Lare
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                       Bradypodion.
NCBI_TaxID=179888;
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AAS16521;
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106-1197
10 OG-1197
10 OS-41
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ID AAS1
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MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                                                                       Snyder L.A., Davies J.K., Saunders N.J.;
"Microarray genomotyping of key experimental strains of Neisseria
gonorrhoea reveals gene complement diversity and five new neisserial
genes associated with Minimal Mobile Elements.";
BMC Genomics 5:23-23(2004).
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Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
NCBI TaxID=78584;
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                                                                                                                                                      Neisseria gonorrhoeae.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.9%; Score 24; DB 2; Length 10; 60.0%; Pred. No. 3.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIKAAINENSII;
Snyder L.A.S., Davies J.K., Saunders N.J.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY386266; AAS16521.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 10 AA; 1227 MW; BACCBB286379D1A6 CRC64;
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27, Created)
27, Last sequence update)
27, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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SEQUENCE 9 AA; 1174 MW; 16C563636B5045B0 CRC64;
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                                                                                                                                                                                                              Neisseriaceae, Neisseria.
NCBI_TaxID=485;
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Matches 3; Conservative
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MEDLINE=21184272; PubMed=11286490;
Pastcrini J., Martin R.D., Ehresmann P., Zimmermann B., Forstner M.R.;
"Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Strepsirhini, Cheirogaleidae,
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                                                                                                                                                   Score 23.5; DB 2; Length 9;
Pred. No. 1.8e+06;
0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
02-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit III (Fragment)
Name=COIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Cytochrome oxidase subunit III (Fragment).
                                                                                                  D5C563636B5045A2 CRC64;
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EMBL; AF224637; AAK70599.1; --
EMBL; AF224638; AAK70699.1; --
EMBL; AF224639; AAK70603.1; --
EMBL; AF224639; AAK70607.1; --
EMBL; AF224639; C:mitochondrion; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
NON TER 1
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01-DEC-2001 (TrEMBLrel. 19, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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                                                                                                                                                         42.0%;
                                                                                                  SEQUENCE 9 AA; 1160 MW;
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Microcebus ravelobensis.
Mitochondrion.
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Best Local Similarity
4; Conserv?
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SEQUENCE
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MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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Pastorini J., Forstner M.R., Martin R.D.;
"Phylogenetic relationships among Lemuridae (Primates): evidence from
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
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Pastcrini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M wholecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences ";
Mol. Phylogenet. Evol. 19:45-56(2001).
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Mammalia; Eutheria; Primates; Strepsithini; Daubentoniidae;
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Pred. No. 1.8e+06;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
Name-COIII;
                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
                                                                                                                                                                                                                   Name=COIII;
Lepilemur edwardsi (Milne-Edwards's sportive lemur)
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA; 1160 MW; D5C563636B5045A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
EMBL; AF224595; AAP33644.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
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EMBL, AF224641; AAK70615.1; -.
EMBL; AF224642; AAK70619.1; -.
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=122230;
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094NA9
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SEQUENCE FROM N.A.
MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                          Forstner M.R.;
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SEQUENCE FROM N.A.
MEDILINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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                                                                                      SEQUENCE FROM N.A.
MEDLINE=21184272; PubMed=11286490;
Pastcorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.
Wholecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
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MEDLINE=21184272; PubMed=11286490;
MEDLINE=21184272; PubMed=11286490;
Pastorini J., Martin R.D., Ehreemann P., Zimmermann E., Forstner M. "Molecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
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Mammalia, Eutheria, Primates, Strepsirhini, Cheirogaleidae,
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Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
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Pred. No. 1.8e+06;
0; Mismatches 0; Indels
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9 AA; 1160 MW; D5C563636B5045A2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003)
EMBL, AF224630; AAK706571.1; -.
EMBL, AF224631; AAK706575.1; -.
GO, GO:0005739; C:mitochondrion; IEA.
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EMBL; AF224624; AAK70547.1; -
EMBL; AF224626; AAK70551.1; -
EMBL; AF224626; AAK70555.1; -
EMBL; AF224677; AAK70559.1; -
EMBL; AF224629; AAK70563.1; -
EMBL; AF224629; AAK70563.1; -
GO; GO:0005739; C:mitochondrion; IEA.
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                                         NCBI_TaxID=122231;
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Mitochondrion.
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Paraneoptera, Hemiptera, Euhemiptera, Heteroptera, Panheteroptera, Pentatomomorpha, Pentatomoidea, Pentatomidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.0%; Score 23.5; DB 2; Length 9; 57.1%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                         Indels
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h 42.0%; Score 23.5; DB 2; Similarity 57.1%; Pred. No. 1.8e+06; 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tectocoris diophthalmus (cotton harlequin bug).
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Q94XE;
01-DEC-2001 (TEMBLE1. 19,
01-DEC-2001 (TEMBLE1. 19,
01-JUN-2003 (TEMBLE1. 24,
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version 5.1.6
- 2004 Compugen Ltd.
GenCore (c) 1993
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US-10-046-922-34 56 1 XGYWLTIWGX 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s: geneseqp2000s: geneseqp2001s: geneseqp2001s: geneseqp2002s: geneseqp2003bs: geneseqp2003bs: geneseqp2003bs: A Geneseq 23Sep04:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ion	VEGFR	ΛEG	Fc region	Hun	Pro	E. faeciu	Human HIV	Human ATP	Mouse ATP	A human M	Human ATP	Human ATP	Human ATP	Human ATP	Human	Human ATP	Human ATP	Human ATP	Homo sapi	Fc region	Human ser		Peptide #	Human bon	Human bra
Description	Abp53931	Abp53932	Aao26093	Adj 50760	Abu30004	Adc97318	Aab62747	Aae09365	Aae09362	Aay43544	Aae09361	Aae09370	Aae09367	Aae09368	Aae09369	Aae09364	Aae09371	Aae09363	Abp52113	Aao26134	Adj50801	Abb38460	Aam31901	Aam71604	Aam59071
Ω	ABP53931	ABP53932	AA026093	ADJ50760	ABU30004	ADC97318	AAB62747	AAE09365	AAE09362	AAY43544	AAE09361	AAE09370	AAE09367	AAE09368	AAE09369	AAE09364	AAE09371	AAE09363	ABP52113	AA026134	ADJ50801	ABB38460	AAM31901	AAM71604	AAM59071
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Query Match	96.4	96.4	76.8	76.8	76.8	76.8	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	ഥ	75.0	75.0	75.0	75.0	73.2	73.2	73.2	73.2	73.2	73.2
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The present invention describes an isolated peptide (I) that binds to and

Claim 12; Page 80; 149pp; English.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Abg51286 Human liv Abg41416 Human pep Aay00213 Enterococ Abp41432 E faecali Abu13711 Enterococ Adh8745 Enterococ Adh8745 Enterococ Aby13712 Enterococ Aby13710 Enterococ Aby13710 Enterococ Aby13710 Enterococ Adn46152 Thermococ Adn46151 Thermococ Adn46151 Thermococ Adn46151 Thermococ Adn46151 Thermococ Adn46151 Thermococ Adn46151 Thermococ Adn46171 Thermococ Adn4617 The	Η ΙΙ Σ
ABG53286 ABG41416 AAY00213 ABA93432 ABU88460 ABU3711 ABP63431 ABP63431 ABP63431 ABP63431 ABR6152 ABR613710 ADR46152 ABR027261 ABC77263	ABO27255 ABO27255 ABO27277 ABO27273
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ALIGNMENTS

RESULT 1

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Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypetrension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                           'note= "any amino acid"
                                                                                                                                                                                                                                      'note= "any amino acid"
                                                                           VEGFR-3 binding peptide SEQ ID NO:34.
                                                                                                                                                                                                      Location/Qualifiers Misc-difference 1
        ABP53931 standard; peptide; 10 AA.
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                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                        25-JUL-2002.
                                                     09-JAN-2003
                                                                                                                                                                                           Synthetic.
                                ABP53931;
ABP5393
          CXSXLTTTXBXBXBXBXBXBXTTTTTXSSXXXXXXXBXBXCXCXCC
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         have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, bancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, osesphagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
 endothelial growth factor receptor 3 (VEGFR-3). (I)
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                                                                                                                                                                                                                                                                                                    96.4%; Score 54; DB 5; Length 10; 100.0%; Pred. No. 0.091; ive 0; Mismatches 0; Indels
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      pancress, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel isolated polypeptides comprising a sequence that binds an immunoglobulin Fc region. The polypeptides are useful as binding molecules for detecting, isolating or purifying immunoglobulin Fc-region polypeptides present in a solution, e.g. whole blood, plasma or transgenic milk. The Fc-region binding polypeptides are also useful for regulating or preventing an antibody response, or for increasing the half-life and over all stability of a therapeutic or diagnostic compound that is administered to or enters the circulatory system of an individual. This sequence represents an Fc region binding
                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk; antibody response; half-life; stability; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides, useful as binding molecules for detecting, isolating purifying immunoglobulin Fc-region polypeptides present in a solution, for regulating or preventing an antibody response.
                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potter MD;
spleen, kidney, lymph node, small intestine, blood cells
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                                                                                                                                      DB 5; her.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
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                                                                                                                                                                            0; Mismatches
                                                                                                                                                 Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    Fc region binding peptide SEQ ID No 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stochl M,
                                                                                                                                                                                                                                                                                                             AAO26093 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 76; 152pp; English.
                                                                                                                                                 96.4%; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2002; 2002WO-US012492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2001; 2001US-0284534P.
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                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide of the invention
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                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu 0,
                                                                                                                                                                                                           GYWLTIWG
                                                                                                                                                                                                                                        GYWLTIWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DYAX-) DYAX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 AA;
                                                                                                                     Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200286070-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                       03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rondon IJ,
                                                                                                                                                                                                                                                                                                                                            AA026093;
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Matches
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03-OCT-2002
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Wall D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of evaluating sample by providing a soluble serum protein (I), one or more compounds physically associated with (I), and a (I)-binding agent that comprises a peptide that specifically binds to (I), allowing the (I)-binding agent to bind to to form a complex including one or more compounds physically associated with (I), separating the complex from one or more components of the sample, and evaluating one or more of the physically associated compounds. The sample comprises blood or serum, or is obtained from a biopsy. The sample may also be obtained from a tumour or a region within modulate interaction of serum protein-binding compound and serum protein and for identifying binding ligands for serum protein. The present sequence represents a serum albumin-binding peptide identified using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evaluating sample comprising soluble serum protein by forming complex comprising serum protein and physically associated compounds using peptide ligand that specifically binds with proteins, which is separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 8; Length 13; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                           human serum albumin; HSA; serum; blood; tumour; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #15531.
                                                                                                                                                                                                                                 Human serum albumin binding peptide, Seg ID No 297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 297; 191pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU30004 standard; protein; 474 AA
                                                                                                       ADJ50760 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-2003; 2003WO-US018896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-2002; 2002US-0388642P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.8%;
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GYWCNVWG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-082161/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYWLTIWG 9
  GYWCNVWG 8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                         06-MAY-2004
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                                                                                                                                                 ADJ50760;
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ID ABU3
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AC ABU
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the foll antiennes esquences given in the appecification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid concluded are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that thas an activity against a hilloence the activity of the gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) identifying a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibicit; (10) profiling a compound activity; (11) a culture comprising strains in which the gene or underexpressed, (12) determining the extent compound; a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or product is overexpressed or underexpressed; (12) determining the extent compound; or (13) identifying the target of a compound that inhibits the compound that inhibits the compound that inhibits or collection of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for dend discovery proprises.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of
Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or e
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 57928; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SEZ-2001; 2001US-00948993.
25-GCT-2001; 2001US-0342939.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC.
                                                                                   Enterococcus faecium.
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Trawick JD,
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N-PSDB; ACA33874.
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Best Local Similarity
Matches 6; Conserv
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RESULT 6

ADC97318

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The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gpl20. These can be used in diagnosis and therapy of HIV-1 infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gpl20, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1 infected mammal.
                                                                                                                       Human immunodeficiency virus-1; HIV-1; human monoclonal antibody; envelope glycoprotein; gp120; diagnosis.
                                                                                  Human HIV-1 monoclonal antibody SEQ ID NO: 46.
                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 51-52; 81pp; English.
                                                                                                                                                                                                                                                                                                                              23-JUN-2000; 2000WO-US017327.
                                                                                                                                                                                                                                                                                                                                                                          99US-0141701P
                                         03-APR-2001 (first entry)
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N-PSDB; AAF29048.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          30-JUN-1999;
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                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watkins BA,
                                                                                                                                                                                                                                                                                   04-JAN-2001
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AAB62747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid derived from
Enterococcus faceium encoding an Enterococcus faceium polypeptide having
One of 10 fully defined sequences given in the (or comprising 40
sequential nuclectides chosen from any of the nucleic acids, its
complement or sequences hybridising to it). Also included are a
recombinant vector comprising the nucleic acid operably linked to
transcription regulatory element, a cell comprising the vector and a
single-stranded probe comprising the nucleic acid. The nucleic acids are
chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
The nucleic acids is useful for diagnosing pathological conditions
resulting from E. faceium bacterial infection (e.g. urinary tract
infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
infection, and for screening drugs such as agonists and antagonists. The
nucleic acid is useful for recombinant production of Candida albicans
derived peptides or antisense polypeptides. Pharmaceutical compositions
and vaccines containing the nucleic acid are useful for preventing or
treating Enerococcus faccium infections. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid derived from Enterococcus faecium encoding e
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                         Vaccine, urinary tract infection, bacteraemia, endocarditis, wound, abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 7; Length 492;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 6945; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               one if the disclosed E. faecium proteins.
                                                                                                                                                                                                E. faecium protein sequence SEQ ID 6945
                                                             ADC97318 standard; protein; 492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0051571P.
98US-0085598P.
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00107532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doucette-Stamm L.A, Bush D;
                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                            Enterococcus faecium
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Best Local Similarity
6; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYWLTCW 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-799836/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYWLTIW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADC93664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-1998;
                                                                                                                                                     01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                     US6583275-B1
                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection.
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                                                                                                         ADC97318;
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                                                                                                                                                                                                                                                                                 Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistence-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXB; heritable disorder; retinal haemorrhage;
                              Gaps
                                                                                                                                                                                                                                                     Human ATP-binding cassette transporter ABCC6, MRP6 truncated mutant.
                              ..
0
75.0%; Score 42; DB 4; Length 120; 62.5%; Pred. No. 65; ive 2; Mismatches 1; Indels
                                                                                                                                                                AAE09365 standard; protein; 1140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-2001; 2001WO-US005741.
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AAB62747 standard; protein; 120 AA.

AAB62747 ID AAB6 XX

RESULT 7

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Terry S;

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Claim 10; Page; 163pp; English.
    23-FEB-2000; 2000US-0184269P
                                                                                                                                                                                                                                         19-NOV-2001 (first entry)
                                                                                                                                                                                  Best Local Similarity 71.4
Matches 5; Conservative
                       Boyd CD, Csiszar K,
                                                                                                                                                                                                   ||||::|
965 GYWLSLW 971
           (PXEI-) PXE INT INC
               (UYHA-) UNIV HAWAII
                              WPI; 2001-536645/59
                                                                                                                                                                                              2 GYWLTIW 8
                                                                                                                                                                       Sequence 1140 AA;
                                  N-PSDB; AAD16258
                                                                                                                                                                                                                                 AAE09362;
                                                                                                                                                                               Query Match
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Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid. Urban Z, Example 5; Page 152-159; 163pp; English Lesaux O, 23-FEB-2001; 2001WO-US005741. 23-FEB-2000; 2000US-0184269P. Ouery Match Best Local Similarity 71.4%, 26-JAN-2000 (first entry) Csiszar K, 996 GYWLSLW 966 2001-536645/59 PXEI-) PXE INT INC UYHA-) UNIV HAWAII 2 GYWLTIW 8 Sequence 1498 AA; WPI; 2001-536645/ N-PSDB; AAD16236. 30-AUG-2001. Boyd CD, AAY43544; RESULT 10 AAY43544 ð 셤 The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a CPXE mutation. Mutations associated with PXE maps to the ATP-binding CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane-spanning composition to three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular C degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 allels who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are consentling in view of the PXE status. The methods are useful for cuseful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) truncated mutant which is obtained as the creall of a stop codon at position 1141 of MRP6 protein. Note: The human ATP-binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: human ATP-binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: human ATP-binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: human ATP-binding variet transporter ABCC6 (MRP6) protein [SED ID NO: human ATP-binding variet transporter ABCC6 (MRP6) protein [SED ID NO: human ATP-binding variet vari ô Mouse; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; whitifarug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage. Screening presence of Pseudoxanthoma elasticum mutation useful for identifying homozygotes, compound heterozygotes or carriers involves determining presence of mutation in MRP6 (ABCC6) nucleic acid. Gaps ö Mouse ATP-binding cassette transporter ABCC6 (MRP6) protein. 75.0%; Score 42; DB 4; Length 1140; 71.4%; Pred. No. 5.9e+02; ive 2; Mismatches 0; Indels Terry S; Urban Z, AAE09362 standard; protein; 1498 AA. Lesaux O,

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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a CX MED with the AXP-binding composition. Mutations associated with PXE maps to the AYP-binding composition. Mutations associated with PXE maps to the AYP-binding composition on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane-spanning chalces grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retinal hamile and less of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with appropriate genetic counselling in view of the PXE status. The methods are useful for counselling in view of the PXE status. The methods are useful for the identifying homozygotes, compound heterozygotes or carriers and thus are diagnosis. The present sequence is mouse ATP-binding casestte (ABC) transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since Desire and an area of genetic and an area of genetic and an area of genetic and an area of an area of genetic and an area of ge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 42; DB 4; Length 1498; 71.4%; Pred. No. 7.7e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; MPR-related ABC transporter; MOAT protein; MOAT-E; MOAT mediated transport; anticancer drug sensitivity; transporter mediated cellular efflux; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A human MPR-related ABC transporter designated MOAT-E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Resistance associated protein 6 (MRP6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY43544 standard; protein; 1503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THXSXXXXXXXXXXXXX
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WO200162977-A2 Mus musculus,

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Example 2; Fig 3; 163pp; English.
                                                                                                                                                                                                                                Lesaux O,
                                                                                                                                                    23-FEB-2001; 2001WO-US005741.
                                                                                                                                                                          23-FEB-2000; 2000US-0184269P
                                                                                                                                                                                                                                                     WPI; 2001-536645/59.
N-PSDB; AAD16230, AAD16231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                Csiszar K,
                                                                                                                                                                                               (PXEI-) PXE INT INC. (UYHA-) UNIV HAWAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||::|
965 GYWLSLW 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GYWLTIW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1503 AA
                                                                                                           WO200162977-A2
                                                                                                                                30-AUG-2001
                                                                                                                                                                                                                                Boyd CD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE09370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                Region
           Region
                                                     Region
                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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 HXXX
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                                                                                                                                                                                                                                                                                                       The present sequence represents a human MPR-related ABC transporter (MOAT) protein, designated MOAT-E. The protein comprises a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, having Walker A and B ATP binding sites and several potential membrane spanning domains. The MOAT nucleic acids are useful for screening a test compound for inhibition of MOAT mediated transport, indicated by restoration of articancer drug sensitivity, which in turn causes a reduction of transporter mediated collular efflux of anticancer agents. MOAT DNA or RNA may be used as probes to detect the presence or expression of genes encoding MOAT proteins. Anti-MOAT antibodies are useful for detecting and quantitating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6; Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            656. .679
/note= "Nucleotide binding fold-1 (NFB-1) region"
747. .768
                                                                                                                                                                                                                                                                New transporter gene useful for screening for anti-cancer drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ATP-binding cassette transporter ABCC6 (MRP6) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%; Score 42; DB 2; Length 1503; 71.4%; Pred. No. 7.7e+02; ive 2; Mismatches 0; Indels
                    'note= "encoded by TGC"
                                          'note= "encoded by TTC"
/note= "encoded by ACT"
                                                                /note= "encoded by CCC"
                                                                                                                                                                                                                                                                                      Claim 39; Page 144-147; 153pp; English.
                                                                                                                                                                                                           Lee K, Belinsky M, Bain L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE09361 standard; protein; 1503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                      (FOXC-) FOX CHASE CANCER CENT
                                                                                                                                 99WO-US006644.
                                                                                                                                                    98US-0079759P.
98US-0095153P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 71.4
           Misc-difference 1274
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965 GYWLSLW 971
                                                                                                                                                                                                                                WPI; 1999-610812/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1503 AA;
                                                                                                                                                                                                                                            N-PSDB; AAZ30081
                                Misc-difference
                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOAT proteins
                                                                                                                                 26-MAR-1999;
                                                                                                                                                                 03-AUG-1998;
                                                                                     WO9949735-A1
                                                                                                                                                      27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE09361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                           Kruh G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6 maps to the ATP-binding cassette transporter ABCC6 (MRP6 maps as a persence of a protein located in the plasma membrane containing 17 membrane - spanning chelices grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retinal haemorrhages leading to macular cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are constituted managements. ABCC6 (MRP6) protein belonging to sub-family "C". Since Pacific Fames associated managements and managements associated managements as a special managements. ABCC6 (MRP6) protein for managements it is also called Multidrug propriet and managements associated managements as managements as associated managements.
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/note= "Nucleotide binding fold-1 (NFB-1) region"
775. .784
/note= "Nucleotide binding fold-1 (NFB-1) region"
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                                                                                                                                                                                                                                                                                                                                                                  /note= "Nucleotide binding fold-2 (NFB-2)
                                                                                                                                                                                   (NFB-2)
                                                                                                                                                                                                                                                                             (NFB-2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Urban 2, Terry S;
                                                                                                                                                                                                                                       1321. .1327
/note= "Nucleotide binding fold-2
1403. .1433
                                                                                                                                                                                   /note= "Nucleotide binding fold-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 42; DB 4; Le 71.4%; Pred. No. 7.7e+02; Live 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Resistance associated protein 6 (MRP6)
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Multidrug Resistance-associated protein 6; macular degeneration; ABCC6; ATP-binding cassette transporter; arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;

mutant; mutein.

sapiens.

Homo

Synthetic.

/note= "Wild type Val substituted with Phe"

Location/Qualifiers

Misc-difference 1298

WO200162977-A2

30-AUG-2001.

ŝ Terry

Urban Z,

Lesaux O,

Csiszar K,

Boyd CD,

PXEI-) PXE INT INC (UYHA-) UNIV HAWAII WPI; 2001-536645/59.

N-PSDB; AAD16260

23-FEB-2001; 2001WO-US005741. 23-FEB-2000; 2000US-0184269P.

Human ATP-binding cassette transporter ABCC6 (MRP6) V1298F mutant.

(first entry)

19-NOV-2001

AAE09367;

AAE09367 standard; protein; 1503 AA

RESULT 13

AAE09367

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Homo sapiens.
19-NOV-2001
                30-AUG-2001
         Synthetic
                                                        Query Match
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding Cassette transporter ABCC6 (MRP6 page encodes a 165 kba protein located in the plasma membrane containing 17 membrane spanning helices grouped into three transmembrane domains. PXE is inherited as an eutosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with a heritable disorder characterised by mineralisation of elastic fibers in skin, arteried and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of candiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) R1314W mutant protein. Note: The present sequence is human apportent is derived from human ATP-binding cassette transporter ABCC6 (MRP6) protein (ABE09361)
                                                                                                                                                                                     Human, prenatal diagnosis, dermal lesion, cardiovascular disease, MRP6, Multidrug Resistance-associated protein 6, macular degeneration, ABCC6, ATP-binding cassette transporter, arterial insufficiency; chromosome 16; Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage,
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The invention relates to methods and compositions for diagnosing and treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6 maps to the ATP-binding consette transporter ABCC6 (MRP6 maps associated protein cassette transporter ABCC6 (MRP6) gene encodes a 165 kba protein located in the plasma membrane containing 17 membrane - spanning chalces grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characteried by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, associated MRP6 alleles who are then provided with appropriate genetic degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE individuals in view of the PXE status. The methods are useful for counselling in view of the PXE status. The methods are useful for disanosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) protein. Note: The present conditional cassette transporter abcc6 (MRP6) protein. Note: The present fransporter faint of ABCC6 (MRP6) protein. Note: The present france is not shown in the specification but is derived from human ATP-finner 3 of the present protein. ABCC6 (MRP6) protein. Note: The present protein and present fransporter. ABCC6 (MRP6) protein (SED ID NO: 3) shown in the specification of the protein (ABCD).
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Gaps

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75.0%; Score 42; DB 4; Length 1503; 71.4%; Pred. No. 7.7e+02; ive 2; Mismatches 0; Indels

Best Local Similarity 71.4 Matches 5, Conservative

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             Score 42; DB 4; Length 1503; Pred. No. 7.7e+02;
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Matches 5; Conservative
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useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (WRP6) G1302R mutant protein. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (WRP6) protein [SED ID NO: 3] shown in figure 3 of the specification (AAB09361)
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skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counsalling in view of the PXE status. The methods are useful for identifying homozygotes, compound heteroxygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prematal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) Al303P mutant protein. Note: The present sequence is hown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in figure 3 of the specification (AAE09361)
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Sequence 1503 AA;

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Sequence 6945, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES; 7310
CORRESPONDENCE ADDRESS;
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COPERATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1999
ATTORNEY/AGRYI INFORMATION:
                   US-08-462-109A-6
US-08-463-109A-6
US-08-461-384B-6
US-08-461-384B-2
US-08-463-092B-2
US-08-463-092B-2
US-08-463-109A-2
US-08-460-907B-2
US-08-460-907B-3
US-08-461-1384B-2
US-08-461-384B-2
US-08-461-384B-2
US-08-461-384B-4
US-08-461-384B-4
US-08-461-384B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEFAX: (781)893-8077
INFORMATION FOR SEQ ID NO: 6945:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...492
; SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945
                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                               STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 492 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
 ORIGINAL SOURCE
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US-09-134-000C-3630

US-09-134-000C-3630

US-09-134-000C-3630

Patent No. 6617156

GENERAL INFORMATION:

TITLE OF INVERMION:

THERAPEUTICS

TH
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: ROCKVILLE
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 4; Length 222;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                            COUNTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/071,035

FILING DATE:
CLASSIFICATION DATA:

APPLICATION NUMBER: BS00/68

PREGISTRATION NUMBER: BB369P2

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes

REGISTRATION NUMBER: 98369P2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514

TELEPAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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; ORGANISM: Enterococcus faecalis
US-09-134-000C-3630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.2%;
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Best Local Similarity 62.5%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 62.5
Local 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-09-071-035-408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 GTWITLWG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GYWLTIWG 9
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                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-792-616-9
Sequence 9, Application US/09792616
Facent No. 6780587
GENERAL INFORMATION:
APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Pseudoxanthoma Elaeticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
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Parent No. 6780587

GENERAL INFORMATION:
APPLICANT: PXE INternational, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
TITLE REPERENCE: PXE-001
TITLE REPERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%; Score 42; DB 4; Length 1498; 71.4%; Pred. No. 2.8e+02;
                                                    DB 4; Length 492;
66;
                                                                                                              1; Indels
                                                                                                           0; Mismatches
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                                                       Score 43;
Pred. No. 6
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; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INPORMATION:
                                                       76.8%;
                       Query Match
Best Local Similarity 85...
6. Conservative
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Matches 5, Conservative
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ORGANISM: Homo sapiens
US-09-792-616-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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965 GYWLSLW 971
                                                                                                                                                                  2 GYWLTIW 8
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                    ô
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                                                                                                  Score 40; DB 4; Length 668;
Pred. No. 2.4e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7310
CORRESPONDENCE BADDRESSE:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 69.6%; Score 39; DB 4; I Local Similarity 71.4%; Pred. No. 2.5e+02; Pees 5; Conservative 1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 14 July 2, 1997
ATTORNEY/AGBNT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 47,489
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature;
; LOCATION: (B) LOCATION 1...478
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:
US-09-107-532A-6868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                           Sequence 6868, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6868:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
STATE: Massachusetts
                                                                                                           71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                      ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                         Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 GYWLSAW 104
                                                                                                                                                                                                                         372 YWMTIW 377
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                                                                                                                                                                                           3 YWLTIW 8
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  LENGIH: 668
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Matches
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Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
SEQ ID NO 19350
                                                                                                  US-09-071-035-406

Sequence 406, Application US/09071035

Sequence 406, Application US/09071035

Sequence 406, Application US/09071035

Patent No. 6448043

TITLE OF INTERNITY Gil H. Choi

TITLE OF INTERNITY H. Choi

TITLE OF INTERNITY H. Choi

TORRESPONDENCE ADDRESS:

ADDRESSE: Human Genome Sciences, Inc.

STRET: Rockville

CITY: Rockville

STATE: Maryland

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATION SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: FELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 406:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-071-035-406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |:|:||
203 GTWITLWG 210
203 GTWITLWG 210
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US-09-248-796A-19350
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22785
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (6),(77),(85)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknov
US-09-248-796A-22785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 4; Length 132;
; Pred. No. 1.4e+02;
0; Mismatches 0; Indels
  Score 37; DB 4; Length 24;
Pred. No. 26;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Thurmond, Jennifer
APPLICANT: Kirchner, Stephen J.
APPLICANT: Rirchner, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
FILE REFERENCE: 6407.US.01
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.1%; Score 37; 100.0%; Pred. No.
                                                                                                                                                                                                                   US-09-248-796A-22785
; Sequence 22785, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09145828A Patent No. 6403349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Caenorhabditis elegans
  h 66.1%;
Similarity 57.1%;
4; Conservative
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Best Local Similarity 57.14
E. Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                 :||::||
16 HWLSLWG 22
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Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                        3 YWLTIWG 9
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SEQ ID NO 11
LENGTH: 278
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                                                       Sequence 2629, Application US/09540236

Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: GATY G.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2005-001
CURRENT PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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Fatent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT PILION NUMBER: US/09/270,767

CURRENT PILION DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 4173

LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62317
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56389
LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.1%; Score 37; DB 4; Length 24; 57.1%; Pred. No. 26; 0; Indels ive 3; Mismatches 0; Indels
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; Sequence 56389, Application US/09270767
; Patent No. 6703491
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US-09-270-767-56389
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.3
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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US-09-540-236-2629
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GOWLTLW 122
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16 HWLSLWG 22
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Best Local Similarity
Matches 4; Conserv
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                                              US-09-540-236-2629
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Job time : 24.0189 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                           RESULT 14
US-09-903-456-18
Sequence 18, Application US/09903456
Sequence 18, Application US/09903456
Sequence 18, Application US/09903456
Sequence 18, Application US/09903456
APPLICANT: Aboott Laboratories
APPLICANT: Headip
APPLICANT: Headip
APPLICANT: Headip
APPLICANT: Headip
APPLICANT: Headip
APPLICANT: Bereira, Suzette L
ITILE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407 US. P3
CURRENT APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 2000-07-24
PRIOR PLING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR PLING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/145,828
PRIOR PLING DATE: 1999-00-02
NUMBER OF SEQ ID NOS: 116
SOCTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 18
LENTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18
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US-09-252-991A-23328
108 GYWIFLW 114
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|111 GYWISAW 117
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US-09-252-991A-23328
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Search completed: December 30, 2004, 13:19:19

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Sequence 406, App Sequence 1966, App Sequence 1, Appli Sequence 5, Appli Sequence 9, Appli Sequence 9, Appli

Sequence 13, Sequence 17,

US-09-071-035-408

US-10-206-576-408

US-09-071-035-408

US-09-071-035-408

US-09-910-483-1

US-09-910-483-2

US-09-910-483-2

US-09-910-483-3

US-09-910-483-4

US-10-160-232-86

US-10-125-869A-75

US-10-1424-599-226815

US-10-160-262-65-178

Sequence 408, App Sequence 408, App Sequence 406, App

Sequence 17, Appl Sequence 21, Appl Sequence 29, Appl Sequence 33, Appl Sequence 31, Appl Sequence 41, Appl Sequence 61, Appl Sequence 90, Appl Sequence 90, Appl Sequence 299, Appl Sequence 126815, Sequence 1364, Appl Sequence 13667, Sequence 1376, Appl Sequence 5178, Appl Sequence 51780, Appl

US-10-282-122A-52805 US-10-282-122A-57680 US-09-738-626-4579 US-10-425-115-260407

ALIGNMENTS

US-10-091-007-88

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Sequence 34 Application US/10046922

Publication No. US20020164667A1

GENERAL INPORMATION:

APPLICANT: Alitalo, Kari

APPLICANT: Koivunen, Erkki

APPLICANT: Koivunen, Erkki

APPLICANT: Koivunen, Erkki

APPLICANT: Koivunen, Erkki

PILE REFERENCE: 28967/37084A

CURRENT FILING DATE: 2002-01-15

CURRENT FILING DATE: 2002-01-15

WUMBER OF SEQ ID NOS: 80

SOFTWARE: Patentin version 3.0

SEQ ID NO 34

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.4%; Score 54; DB 13; Length 10; 100.0%; Pred. No. 0.22; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: isolated peptide
FEATURE:
NAME/KEY: SITE
COCHION: (1)...(1)
COTHER INFORMATION: X is any amino acid
LOCATION: (10)...(10)
COTHER INFORMATION: X is any amino acid
US-10-046-922-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Sequence 73, Appl
Sequence 297, Appl
Sequence 190740,
Sequence 9, Appli
Sequence 9, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 114, Appl
Sequence 114, Appli
Sequence 138, Appli
Sequence 338, Appli
Sequence 338, Appli
Sequence 338, Appli
Sequence 338, Appli
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                                                                                           December 30, 2004, 13:08:04 ; Search time 74.5283 Seconds (without alignments) 48.267 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/NCT NEW PUB. Pep:*

2: /cgn2_6/ptodata/1/pubpaa/RCT NEW PUB. Pep:*

4: /cgn2_6/ptodata/1/pubpaa/NCG NEW PUB. Pep:*

5: /cgn2_6/ptodata/1/pubpaa/NSG NEW PUB. Pep:*

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9: /cgn2_6/ptodata/1/pubpaa/NSG PUBCOMB. Pep:*

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11: /cgn2_6/ptodata/1/pubpaa/NSG PUBCOMB. Pep:*

12: /cgn2_6/ptodata/1/pubpaa/NSG PUBCOMB. Pep:*

13: /cgn2_6/ptodata/1/pubpaa/NSG PUBCOMB. Pep:*

13: /cgn2_6/ptodata/1/pubpaa/NSG PUBCOMB. Pep:*

14: /cgn2_6/ptodata/1/pubpaa/NSG PUBCOMB. Pep:*

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18: /cgn2_6/ptodata/1/pubpaa/NSIOD_PUBCOMB. Pep:*

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19: /cgn2_6/ptodata/1/pubpaa/NSIOD_PUBCOMB. Pep:*
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(c) 1993 - 2004 Compugen Ltd.
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US-10-046-922-35
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US-10-462-262-297
US-10-462-262-297
US-10-482-122A-57928
US-10-743-28-9
US-09-792-616-9
US-09-792-616-3
US-09-792-792-792-793-3
US-09-864-761-4358
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                                                                                                                                                                                                                                                               1599051 segs, 359727711 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search; using sw model
                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1 XGYWLTIWGX 10
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Match Length
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1498
1503
1503
1503
14
14
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76.8
775.0
775.0
73.2
73.2
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Perfect score:
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                                                                                                                                                                                           Sequence:
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                                                                                                  Run on:
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TITLE OF INVENTION: PROTEIN ANALYSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .cawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                          Sequence 35, Application US/10046922;
Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kidou, Hajime
TITLE OF INVENTION: VEGR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION UNMERR: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 3:
LENGTH: 10
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Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rondon, Isaac Jesus
APPLICANT: Rondon, 1saac Jesus
APPLICANT: Rondon, 1saac Jesus
APPLICANT: Stochl, Mark
APPLICANT: Stochl, Mark
APPLICANT: Ranschoff, Thomas C.
APPLICANT: Ranschoff, Thomas C.
APPLICANT: Ranschoff, Thomas C.
APPLICANT: PALECY INVENTION: DAINGING MOLECTLES FOR FC-REGION
TITLE OF INVENTION: DOLYPEPTIDES
FILE REFERENCE: 3421.1006-001;
CURRENT APPLICATION NUMBER: 06/284,534
PRIOR APPLICANTON NUMBER: 06/284,534
PRIOR PRILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 200
SEQ ID NO 7: SEQ ID NOS: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Fc region binding polypeptide
                                                                                                                                                                                                                                                                                                                                                                                   96.4%; Bccc.
100.0%; Pred. No. v.
0; Mismatches
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APPLICANT: Sato, Aaron K.
APPLICANT: Dawson, Bruce M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 73, Application US/10125869A; Publication No. US20030199671A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35
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Best Local Similarity 100.
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Matches 5, Conservative
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US-10-462-262-297
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                  US-10-046-922-35
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-23
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: immunoglobulin binding polypeptide US-10-462-262-297
FILE REFERENCE: 10280-052001
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT FILING DATE: 2003-06-16
FRIOR APPLICATION NUMBER: US 60/388,642
FRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: PastSEQ for Windows Version 4.0
SERGITH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57928, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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RESULT 9
US-09-792-616-3
US-09-792-616-3
Sequence 3, Application US/09792616
Publication No. US20030165828A1
GENERAL INFORMATION:
APPLICANT: PXE INternational, Inc.;
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing;
TITLE OF INVENTION: Pseudoxanthoma Elasticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
                                                                                                                                               APPLICANT: PXE International, Inc.
APPLICANT: Will be a series of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
TITLE OF INVENTION: Peeudoxanthoma Elasticum
FILE REFERENCE: PXE-001PC
CURRENT APPLICATION NUMBER: US/10/764,328
CURRENT PILING DATE: 2004-01-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1498;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.0%; Score 42; DB 16; Length 14 Best Local Similarity 71.4%; Pred. No. 9.3e+02; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                       Sequence 9, Application US/10764328; Publication No. US20040166521A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Mus musculus
US-10-764-328-9
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 960 GYWLSLW 966
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US-10-764-328-3
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Sequence 190740, Application US/10437963

Seneral Information No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Brabazuk, Brad

APPLICANT: Brabazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants und Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)8

CURRENT APPLICANTON NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 190740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09792616
Sequence 9, Application Wo. US20030165828A1
GENERAL INFORMATION:
APPLICANT: PRE International, Inc.
APPLICANT: PRE International, Inc.
APPLICANT: PREVINCENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing TITLE OF INVENTION: Pseudoxanthoma Elasticum FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
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                                   76.8%; Score 43; DB 15; Length 474;
85.7%; Pred. No. 2.4e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 16; Length 671;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION; Clone ID: PAT_MRT4530_87125C.1.pep
US-10-437-963-190740
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Best Local Similarity 71.4.
                 Query Match
Best Local Similarity 85.
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Best Local Similarity 85.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
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                                                                                                                                                 94 GYWLTCW 100
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US-10-282-122A-57928
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US-09-792-616-9
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OTHER INFORMATION: MAP TO AC000403.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                  75.0%; Score 42; DB 16; Length 1503; 71.4%; Pred. No. 9.3e+02;
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                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    US-10-122-80594-114

Sequence 114, Application US/10125869A

Publication No. US20030199671A1

GENERAL INFORMATION:
APPLICANT: Rondon, Isaac Jesus
APPLICANT: Rondon, Isaac Jesus
APPLICANT: Ley, Arthur C.
APPLICANT: Stochl, Mark
APPLICANT: Potter, M. Daniel (deceased)
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
TITLE OF INVENTION: BOLYPEPTIDES
FILE REFERENCE: 3421.1006-001
CURRENT APPLICATION NUMBER: US/10/125,869A
CURRENT APPLICATION NUMBER: 60/284,534
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 200

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Fc region binding polypeptide US-10-125-869A-114
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Publication No. US20040009534A1

GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Dawson, Bruce M.
TITLE OF INVENTION: PROTEIN ANALYSIS
FILE REFERENCE: 10280-052001
CURRENT APPLICATION WUMBER: US/10/462,262
CURRENT APPLICATION WUMBER: US/10/462,262
CURRENT APPLICATION WUMBER: US/10/462,262

CURRENT FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 430

SOUTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 338
LENGTH: 14
                                                                                                                                                                                                           2; Mismatches
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.5'
                                                                                                                                                                                                             5; Conservative
                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-328-3
                                                                                                                                                                                                                                                                               965 GYWLSLW 971
                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GYWLTIWG 9
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1 GFWCTFWG 8
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US-10-125-869A-114
                                                                1503
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NS-09-864-761-43458

US-09-864-761-43458

Sequence 43458, Application US/09864761

Sequence 43458, Application US/09864761

Sequence 43458, Application US/09864761

Sequence 43458, Application US/09864761

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: HUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR PILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-06-03

PRIOR PELING DATE: 2000-06-03

PRIOR PELING DATE: 2000-06-03

PRIOR PELING DATE: 2000-06-03

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27
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                                                                                                         Length 14;
                                                                                                                                                                             Indels
; OTHER INFORMATION: immunoglobulin binding polypeptide US-10-462-262-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 43458
LENGTH: 34
                                                                                                 Score 41; DB 1; Pred. No. 21; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PLILOR DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                 Query Match 73.2%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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179 GTWITLWG 186
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                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                          linear
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       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-071-035-408
                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                           Sequence 240891, Application US/10424599
; Sequence 240891, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa Thomas J
    APPLICANT: La Rosa Thomas J
    APPLICANT: APPLICANT: APPLICANT: Sov Vinua
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE REFERENCE: 38-21(53223)B
    CURRENT APPLICATION NUMBER: US/10/424,599
    CURRENT FILING DATE: 2003-04-28
    NUMBER OF SEQ ID NOS: 285684
    SEQ ID NO 240891
    LENGTH: B2

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Publication No. US20020045737A1

GENERAL INFORMATION:
APPLICANT: Gil H. Choi

TITLE OF INFORTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:
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                                                                                                                                           Query Match 73.2%; Score 41; DB 9; Length 34; Best Local Similarity 62.5%; Pred. No. 46; Matches 5; Conservative 3; Mismatches 0; Indels
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT3847_59551C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1).:(82)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                   |||:|::|
25 GYWITVFG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                      2 GYWLTIWG 9
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76 GYWLNLW 82
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Best Local Similarity
Matches 5; Conserv
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US-10-424-599-240891
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                                                                         ; OTHER INFORMATIC
US-09-864-761-43458
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US-09-071-035-408
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| PRIOR APPLICATION:
| PRIOR APPLICATION:
| PRIOR APPLICATION NUMBER: |
| APPLICATION NUMBER: |
| ATTORNEY/AGENT INPORMATION: |
| NAME: A. Anders Brookes |
| REGISTRATION NUMBER: 36,373 |
| REFERENCE/DOCKET NUMBER: 98,6372 |
| TELEPHONE: (301) 309-8514 |
| TELEPHONE: (301) 309-8516 |
| TOPOLOGY: innear |
| TOPOLOGY: innear |
| TOPOLOGY: innear |
| TOPOLOGY: innear |
| MOLECULE TYPE: protein |
| SEGULOS TYPE: protein |
| SCONEY MATCH |
| TOPOLOGY: innear |
| MOLECULE TYPE: protein |
| SCONES TYPE: protein |
| TOPOLOGY: innear |
| MOLECULE TYPE: protein |
| SCONES TYPE: protein |
| TOPOLOGY: innear |
| MATCHES |
| TOPOLOGY: innear |
| TOPOLOG
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

Run on:

December 30, 2004, 12:58:17; Search time 11.5094 Seconds (without alignments) 83.598 Million cell updates/sec

US-10-046-922-34 56 1 XGYWLTIWGX 10 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

į		ر حد			SUMMARIES	
Result No.	Score	Match	Length	8	ID	Description
1	42	75.0	441	7	C95307	probable transport
~	42	75.0	1502	~	T42216	multidrug resistan
m	41	73.2	391	7	PC4117	replication protei
4	41	73.2	419	~	E90446	permease [imported
ß	40	71.4	142	~	C34903	•
ø	40	71.4		~	B71038	
7	40	71.4	508	~	C95282	probable ABC trans
&	39	9.69		N	AF1978	hypothetical prote
σ	39	9.69		~	T46745	orni
10	39	9.69		~	C86879	arginine/ornitine
1	38	67.9	118	N	T35739	probable integral
12	38	67.9	426	~	C75176	na+/h+ antiporter
13		67.9	477	~	G90251	ABCTransporter [im
14	38	67.9	583	~	T50103	probable oxidoredu
15	38	67.9	829	~	S58888	Ins P4-binding pro
16	38	67.9	829	~	S71847	Ins P4-binding pro
17	37.5	67.0	1063	~	A33830	cation efflux syst
18	37.5	67.0	1063	N	JC4700	cadmium, zinc, cob
19	37	66.1	123	-	AVMS14	
20	37	66.1	167	~	AF0881	probable exported
21	37	66.1	172	N	AI2232	hypothetical prote
22	37	66.1	187	٦	S13868	
23	37	66.1	197	N	AF2356	hypothetical prote
24	37	66.1	218	7	876385	
52	37	66.1	286	7	E88690	_
56	37	66.1	292	~	849164	Lysk-type protein
27	37	66.1	360	~	S74751	CDP-glucose 4,6-de
28	37	66.1	380	~	S12839	Ig heavy chain pre
53	37	66.1	416	~	AF1127	rod shape-determin

RESULT 2
T42216
multidrag resistance-associated protein homolog MLP-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R;Hirohashi, T42216
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins mair
A;Reference number: Z22081; MUID:98279126; PMID:9614210
A;Accession: T42216
A;Status: preliminary; translated from GB/EMBL/DDBJ

probable amino aci arginine/ornithine arginine/ornitine probable transcarb hypothetical prote phosphatidylglycer partial probable m hypothetical prote 1-acyl-sn-glycerol 1-acyl-sn-glycerol hypothetical prote 1-acyl-sn-glycerol 6PIZ protein - vea	hypothetical prote hypothetical prote YSD83 protein - ye probable membrane
E83497 JH0110 G86878 F82966 F69900 E83140 H85756 G81013 A81957 A61957	A83779 D84541 S43540 B90862
00000000000	0000
4472 4822 1644 1711 2339 2477 2500	292 385 385
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	64.3 64.3 64.3
	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
331 331 332 334 336 44 336 40 40	4 4 4 4 5

ALIGNMENTS

Qy 2 GYWLTIW 8 : Db 92 GYWISIW 98
Query Match 75.0%; Score 42; DB 2; Length 441; Best Local Similarity 71.4%; Pred. No. 32; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
A;Contents: A;Genetics: A;Gene: SMa0684 A;Genome: plasmid C;Superfamily: L-lysine transport protein
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C. A, Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A, Reference number: A96039; MUID:21368234; PMID:11474104
L.; Wyman, W.W.; Jones, T. Savis, N.W.; Diedle, C.; Coucispier; N.W.; Tener, N.W.; Science 293, 668-672, 2001
A; Experimental source: strain 1021, megaplasmid pSymA R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
A:Status: preliminary A:Molecule type: DNA A:Molecule type: DNA A:Residues: 1-441 - KURS A:Resid
A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti A; Reference number: A95262; MUID:21396509; PMID:11481432 A; Accession: C95307
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse, S.; Kalman, S.; Keating, D.H.; Pall, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: C95307
RESULT 1 C95307 probable transport protein SMa0684 [imported] - Sinorhizobium meliloti (strain 1021) maga

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27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                               Query Match
71.4%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 GYWFAYWG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GYWLTIWG 9
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Matches
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A;Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:G
C;Genetics:
A;Molecule type: mRNA
A;Residues: 1-1502 <HIR>
A;Residues: 1-1502 <HIR>
A;Experimental source: strain Sprague-Dawley; liver
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           permease [imported] - Sulfolobus solfataricus
C;Species Sulfolobus solfataricus
C;Species Sulfolobus solfataricus
C;Species Sulfolobus solfataricus
C;Accession: E90446
C;Accession: C;Accession: C;Accession: C;Accession: C;Accession: E90446
C;Accession: E90446
C;Accession: E90446
A;Deffites, A.C; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Farrett, R.A; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A999139
                                                                                                                                                                                                                                                                                                                                                                                                                                 replication protein homolog - Pyrococcus sp. (fragment)
N;Alternate names: hypothetical 391 protein
C;Species: Pyrococcus sp.
C;Species: Pyrococcus sp.
C;Accession: PC4117
R;Rashid, N.; Morikawa, M.; Imanaka, T.
R;Rashid, N.; Morikawa, M.; Imanaka, T.
R;Rashid, N.; Morikawa, M.; Imanaka, T.
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.
A;Reference number: JC4514; MUID:96105215; PMID:8529878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                   Query Match 75.0%; Score 42; DB 2; Length 1502; Best Local Similarity 71.4%; Pred. No. 1e+02; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 2; Length 391;
Pred. No. 41;
0; Mismatches 1; Indels
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Ig heavy chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)
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85.7%;
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A;Residues: 1-391 <RAS>
A;Cross-references: DDBJ:D50018
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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964 GYWLSLW 970
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A; Status: preliminary
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C;Accession: B71038

K;Kavarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic an A;Reference number: A71000; MUID:98344137; PMID:9679194
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A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
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C;Spate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
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Kjarnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowst
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Fittle: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot:
A;Reference number: A95262; MUID:21396509; PMID:11481432
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: NAA
A;Molecule type: NAA
A;Molecule type: NAA
A;Molecule type: NABA
A;Mol
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A;Molecule type: DNA
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probable Na+/H+-exchanging protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
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C; Accession: C34993
R; Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 255, 133-139, 1390
A; Title: Active site structure and antigen binding properties of A; Reference number: A34903; MUID: 90094387; PMID:2104617
A; Accession: C34903
A; Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA
A; Residues: 1-142 < BED>
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argining/ornitine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140]; C,Species: Lactococcus lactis subsp. lactis
C,Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C,Accession: C86879
R,Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001
A;Itle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg. A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86879
A;Cross-references: UNIPROT:Q9CE15; GB:AB005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:GPA;Cross-references: UNIPROT:QCE15; GB:AB005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:GPA;Csperimental source: strain IL1403
C;Genetics: A;Gene: arcDl
C;Superfamily: L-lysine transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable integral membrane protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Spacession: T35739
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.J.
R;Accession: T35739
A;Reference number: Z21588
A;Accession: T35739
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-118 <-SAU>
A;Cross-references uNIPROT:Q9S2K9; EMBL:AL109732; PIDN:CAB52050.1; GSPDB:GN00070; SCOEDE
C;Genetics: Common and Common a
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C751/P
R;anonymous, Genoscope
R;anonymous, Genoscope
A;Date: July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
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C;Superfamily: Streptomyces coelicolor probable integral membrane protein SC7H2.08
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Pred. No. 1e+02;
1; Mismatches 1; Indels
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                                                                                                                                        1; Mismatches
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5; Conservative
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                                                                                                                                        5; Conservative
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FWLSLWG 57
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Matches 5; Conserv
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Science 293, 668-672, 2001
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A,Reference number: A96039; MUID:21368234; PMID:11474104
C;Genetics: A,Genetics: A,G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1377
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; Superfamily: L-lysine transport protein
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C;Species: Lactobacillus sakei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T46745
R;Zuniga, M; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, J. Bacteriol. 180, 4154-4159, 1998
A;Title: Structural and functional analysis of the gene cluster encoding the enzymes of A;Reference number: Z23141; MUD:98361904; PMID:9696763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:053092; EMBL:AJ001330; NID:92764610; PIDN:CAA04686.1; PID:92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein alr1377 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF1978
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.: Kuritz. T.: Sasamoto S. Wartsha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 74;
0; Mismatches 1; Indels
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A;Molecule type: DNA
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Pred. No. 79;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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A; Residues: 1-475 <ZUN>
A; Cross-refe
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-376 <KUR>
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-829 < CUL>
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A;Reference number: A75001
A;Recession: C75176
A;Accession: C75176
A;Accession: C75176
A;Accession: C75176
A;Crossion: DNA
A;Residues: 1-426 «KAW>
A;Cross-references: UNIPROT:Q9V160; GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB4949
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: napA-2; PAB0390
C;Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABCTransporter [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: G90251
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffritss, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable oxidoreductase [imported] - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Species: Schizosaccharomyces pombe
C.Species: Schizosaccharomyces pombe
C.Saccesion: T50103
R.Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
A.Reference number: Z25038
A.Reference number: Z25038
A.Scacesion: T50103
A.Scace
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A;Status: preliminary
A;Status: preliminary
A;Residues: 1-477 <KUR>
A;Cross-references: UNIPROT:Q97ZC3; GB:AE006641; NID:g13814184; PIDN:AAK41270.1; GSPDB:CGGenetics:
A;Genetics:
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66.7%; Pred. No. 1.4e+02;
iive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.9%; Score 38; DB 2; Length 426 Best Local Similarity 62.5%; Pred. No. 1.3e+02; Matches 5; Conservative 1; Mismatches 2; Indels
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Best Local Similarity 75.0%
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Best Local Similarity 66.7°
"--rhes 4; Conservative
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415 WITVWG 420
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Ins P4-binding protein - human (Species: Homo sapiens (man) (Cispecies: Homo sapiens (man) (Cispecies: Homo sapiens (man) (Cispecies: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 04-Apr-2004 (Ciscossion: S58888 (Ciscossion: S58888 (Ciscossion: S58888 (Ciscossion: S58888 (Ciscossion: A.J.; Jackson, T.R.; Dawson, A.P.; Irvi Asture 376, 527-530, 1995 (Ciscossion: A.J.; Jackson, T.R.; Dawson, A.P.; Irvi A;Title: Identification of a specific Ins(1,3,4,5)P(4)-binding protein as a member of the A;Reference number: S58888; WUID:95364929; PMID:7637787
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F;328-539/Domain: ras-specific GAP catalytic domain homology <GAP>
F;571-670/Domain: pleckstrin repeat homology <PLK>
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244 GRWPTIWG 251
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Q74JK6;
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092xf rhizobium m

092xf rhizobium m

09x187 mus musculu

09x187 mus musculu

08225 homo sapien

08225 homo sapien

08225 homo sapien

08725 homo sapien

08728 enterococcu

06cbe4 yarrowia li

09hka9 thermoplasm

097b7 sulfolobus

08dm4 synechococc

07y284 plasmodium

074dr3 geobacter s

Aar14628 geobacter s

Aar14628 geobacter of separation

077557 bordetella
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Q9khq6 bacteroides
O59255 prococcus
Q930n2 rhizobium m
Q88h71 pseudomonas
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Caf21531 corynebac
Q8nqb6 corynebacte
O32816 lactococcus
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Q6mc01 parachlamyd
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                                                                                                                                                                                                                  December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds (without alignments) 62.362 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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              Q8yx40 anabaens ap
Q8xu8 pyrobaculum
Q9xu3 lactococcus
Q6tk71 streptococc
Aar3025 streptoco
G6tk77 bacillus ch
Q73e85 bacillus ch
Aas3409 bacillus
Q81ib bacillus ch
Aas3409 bacillus
Q53092 lactobacci
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anabaena sp
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Bacteria: Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TaxID=33959;
[1]
                                                                                                                                                                                                                                          Lactobacillus johnsonii.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                      ALIGNMENTS
                                                                                  QBIIH9
AAS39409
ARCD LACSK
QBDWP9
      Q6C129
Q8YX40
Q8ZUS8
Q7NSJ2
Q9KGV3
Q6KKV3
Q6KFV3
Q6HP27
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Hemolysin-like protesin.
OrderedLocusNameps=LJ1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AASO8923 PRELIMINARY;
AASO8923;
02-MAR-2004 (TEMBLrel. 27,
02-MAR-2004 (TEMBLrel. 27,
02-MAR-2004 (TEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 YWLSLWG 279
                                                                                                                                                                                                                                                                                                                                             3 YWLTIWG 9
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SEQUENCE FROM N.A.
STRAIN±UWE25;
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SEQUENCE FROM N.A.
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CAF23898
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
05-Numesespoll14,
Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                 Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Prittet A.-C., Zwahlen M.-C., Rouvet M., Altermann B., Barrangou R., Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.; Lactobacillus johnsonii NCC 533."; intestinal bacterium Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

EMBL, AR017203; AAS08923.1; -- SERQUENCE 221 AA; 24721 MW; IDBC78FP9810E152 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
14-pothetical protein OJ1338_B05.118

Name=OJ138_B05.118;
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Spermatophyta; Magnoliophyta; Enbryophyta; Tracheophyta;
Enharcoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                       76.8%; Score 43; DB 2; Length 221; 62.5%; Pred. No. 70; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.8%; Score 43; DB 2; Length 733; 85.7%; Pred. No. 2.1e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Matsumoto T., Katayose Y.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005486; BAC16197.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interero, Misovicia, DUF594.
Pfam; PF04578; DUF594, 1.
Hypothetical protein.
PSEQUENCE 733 AA; 82939 MW; E95884DAD1DC2AC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 AA.
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nes 5; Conservative
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172 GFWLLVWG 179
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Best Local Similarity
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                                STRAIN=NCC 533;
PubMed=14966310;
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"Genome sequence of an amoeba symbiont and its use for reconstructing the evolutionary history of chlamydiae.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX908798; CAF23898.1; -.
Hypothetical protein.
SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-UWE25;
Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U., Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D., Rattei T., Mewes H., Wagner M.; "Genome sequence of an amoeba symbiont and its use for reconstructing the evolutionary history of chlamydiae.";
submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parachlamydia sp. UWE25.
Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
NCBI_TaxID=264201;
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                   Query Match 75.0%; Score 42; DB 2; Length 284; Best Local Similarity 71.4%; Pred. No. 1.3e+02; Matches 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 284;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Probable transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Gaps

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STRAINE-YOR NO. TISSUE LAND.

STRAINE-YOR NO. TISSUE LAND.

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Moore T., Max S.I., Wang J., Halsh P.,

Brownstein M.J., Uddin T.B., Toshlyuki S., Carninci P., Frange C.,

Brownstein M.J., Uddin T.B., Toshlyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaky S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WRPG MOUSE STANDARD; PRT; 1498 AA.

OBALS7; OBOVES6;
01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-family C, member 6).
Name=Abcc6; Synonyms=Mrp6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ddy; TISSUB=Liver; Antohashi T., Sugiyama Y.; Suzoiki H., Hirohashi T., Sugiyama Y.; Mus musculus mRNA for multidrug resistance-associated protein 6 (MRP6), complete cds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%; Score 42; DB 2; Length 1308; 100.0%; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indela
                                                                                                                                                                                                                                                                                                                                                                           1308 AA; 149576 MW; 336120AC8F737AC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                   Pfam; PF00664; ABC membrane; 2.
Pfam; PF00005; ABC tran; 2.
SWART; SW00382; AAA; 2.
PROSITE; PS50929; ABC TMIF; 2.
PROSITE; PS50831; ABC TRANSPORTER 1; 1.
PROSITE; PS50833; ABC TRANSPORTER 2; 2.
ATP-binding.
SEQUENCE 1308 AA; 149576 MW; 336120AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOI=10.1038/mp.a002623.01;
Beck C., Le Saux O., Varadi A., Boyd C.;
"Abcc6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (er) AfCS-Nature Molecule Pages (2004).
                         InterPro; IPR011527; ABC_membrane_1.
InterPro; IPR001140; ABC_TM_transpt.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR003593; AAA ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 685-1498 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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MOUSE
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GO:0005524; F:ATP binding; IEA.
GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO:0000166; F:nuclectide binding; IEA.
GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galibert F., Finan T.M., Cong S.R., Puehler A., Abola P., Ampe F., Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G., Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G., Cowie A., Davis R.W., Dreanc S., Federspiel N.A., Fisher R.F., Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D., Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V., Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B., Ramsperger U., Surzycki R., Thebault P., Vandenbol M., Ver K.-C., Batut J., Yerhe composite genome of the legume symbiont Sinorhizobium meliloti.",
                                                      Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Weils D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
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GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006665; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel_permease1.
InterPro; IPR004841; Permease_region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 2; Length 441;
Pred. No. 1.9e+02;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: Belongs to the ABC transporter family.
EMBL: AF47433; AAL485710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00324; AA permease; 1.
Complete proteome; Plasmid; Transmembrane; Transport.
SEQUENCE 441 AA; 46277 MW; B6F5C9EC96011AD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1308 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21368234; PubMed=11474104;
                                MEDLINE=21396509; PubMed=11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 293:668-672(2001).
EMBL, AE007228; AAK65021.1; -.
PIR, C95307; C95307.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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01-JUN-2002
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Q8T6H2

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DD 01-JU
DD 101-JU
DD

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FUNCTION: May participate directly in the active transport of drugs into subcellular organelles or influence drug distribution indirectly (By similarity). SUBCELLULAR LOCATION: Integral membrane protein (By similarity). SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (Forential).
N-linked (GlGNAC. ..) (Potential).
N-linked (GlCNAC. ..) (Potential).
A -> V (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 (By similarity).
Extracellular (By similarity).
7 (By similarity).
Cytoplasmic (By similarity).
(Cytoplasmic (By similarity).
Extracellular (By similarity).
9 (By similarity).
10 (By similarity).
Extracellular (By similarity).
10 (By similarity).
Extracellular (By similarity).
                                                                                                                                                                                                                                                                                                                      TIGRFAMB; TIGRÓ0957; MRP_assoc_pro; 1.
PROSITE; PS50929; ABC_TMAF; 2.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50831; ABC_TRANSPORTER_2; 2.
ATP-binding; Glycoprotein; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                      2 (By similarity).
Extracellular (By similarity).
3 (By similarity).
Cytoplasmic (By similarity).
4 (By similarity).
5 (By similarity).
5 (By similarity).
6 (By similarity).
7 (Cytoplasmic (By similarity).
7 (Cytoplasmic (By similarity).
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1 (By similarity).
Cytoplasmic (By similarity).
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Cytoplasmic (By similarity).
12 (By similarity).
Extracellular (By similarity).
13 (By similarity).
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15 (By similarity).
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Extracellular (By similarity)
17 (By similarity).
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ABC transporter 1.
ABC transporter 2.
ATP (Potential).
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                                                                                                                                                                                                          MGD; MGI:1351634; Abcc6.
InterPro; IPR00159; AAA ATPase.
InterPro; IPR001140; AAC_TM_transpt.
InterPro; IPR001343; ABC_Transporter.
InterPro; IPR005292; MRP_assoc.
Fram; PP00664; ABC membrane; 2.
Fram; PP00005; ABC membrane; 2.
ProDom; PD00006; ABC transporter; 1.
SWART; SW03382; AAA; 2.
                                                                                                                                                                        EMBL; AB028737; BAA83820.1; -. EMBL; BC049980; AAH49980.1; -.
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531
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                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Multidrug resistance-associated protein 6 (ATP-binding cassette, subfamily C, member 6) (MRP-like protein-1) (MLP-1).
Name-AbcG6; Synonyms=Mrp6, Mlp1;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI _TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- FUNCTION: May participate directly in the active transport of drugs into subcellular organelles or influence drug distribution indirectly (By similarity).
-I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-I- TISSUE SPECIFICITY: High in liver and lower in duodenum and
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Hepatic expression of multidrug resistance-associated protein-like proteins maintained in eisai hyperbilirubinemic rats."; Mol. Pharmacol. 53:1068-1075(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley; TISSUE=Liver;
MaDLINES-20159081, PubMed=-10692506;
Madon J., Hagenbuch B., Landmann L., Meier P.J., Stieger B.;
"Transport function and hepatocellular localization of mrp6 in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=98279126; PubMed=9614210;
Hirohashi T., Suzuki H., Ito K., Ogawa K., Kume K., Shimizu T.,
                                                                                                                                            ;
0
                                                                                                         DB 1; Length 1498;
                                                                                                     Score 42; DB 1; Length 145
Pred. No. 5.9e+02;
2; Mismatches 0; Indels
                                                                      MW; EFCFF33F0EEC813C CRC64;
I -> T (in Ref. 2).
H -> Q (in Ref. 2).
L -> V (in Ref. 2).
N -> S (in Ref. 2).
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EWBL; U73038; AAD12747.1; -
PIR; T42216; T42216.
HSSP; P08716; JMT0.
RGD; 620268; Abcc6.
InterPro; IPR0013593; AAA ATPase.
InterPro; IPR00140; ABC TIM transpt.
InterPro; IPR00140; ABC TIM Eranspt.
InterPro; IPR005329; MRP assoc.
Pfam; PP00664; ABC membrane; 2.
Pfam; PP00005; ABC_tran; 2.
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927 927
1401 1401
1448 1448
1477 1477
1498 AA; 164788 M
                                                                                                         75.0%;
                                                                                                                                            5; Conservative
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960 GYWLSLW 966
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Best Local Similarity
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305255; PT8420; O3UMZ7;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2004 (Rel. 45, Last annotation update)
Multidaug resistance-associated protein 6 (Arp-binding cassette, sfamily C, member 6) (Anthracycline resistance-associated protein)
Multidaug resistance-associated protein)
Multidaug resistance-associated protein)
Name=ABCC6; Synonyms=WRP6, ARA;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Cytoplasmic (By similarity).
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7 (Cytoplasmic (By similarity).
                         Score 42; DB 1; Length 1502;
Pred. No. 6e+02;
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Extracellular (By similarity)
9 (By similarity).
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Extracellular (By similarity)
13 (By similarity).
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Extracellular (By similarity)
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10 (By similarity).
Extracellular (By similarity)
11 (By similarity).
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Cytoplasmic (By Similarity).
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Cytoplasmic (By similarity).
ABC transporter 1.
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ATP (Potential)
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ProDom, PD000006; ABC transporter; 1.
SWART; SM00382; AAA; Z.
FIGRFAMB; TIGR00957; MRP_ABBOC_Dro; 1.
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964 GYWLSLW 970
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MRP6 TUDAN
DO 09525
DT 30-MA
DT 30-MA
DT 30-MA
DT MALLI
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GO:0005624; C:membrane fraction; TAS.
GO:0005886; C:plasma membrane; TAS.
GO:0005224; F:ATP binding; TAS.
GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; TAS.
GO:0005215; F:transporter activity; TAS.
GO:0042493; P:response to drug; TAS.
GO:0006810; P:transport; TAS.
                                                                                                                                                                                                                                                                                           Pfam; PF00664; ABC membrane; 2.
Pfam; PF00065; ABC tran; 2.
Probom; PB000006; ABC transporter; 1.
Probom; PB000006; AAA; 2.
TIGRFAMB; TIGR00957; MRP assoc_pro; 1.
PROSITE; PS50929; ABC TMIF; 2.
PROSITE; PS50931; ABC TRANSPORTER 1; 2.
PROSITE; PS50931; ABC TRANSPORTER 2; 2.
ATP-binding; Disease mutation; Glycoprotein; Polymorphism; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extracellular (By similarity).

1 (By similarity).

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Extracellular (By similarity).

3 (By similarity).

Cytoplasmic (By similarity).

Cytoplasmic (By similarity).

Extracellular (By similarity).

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Extracellular (By similarity).
7 (By similarity).
Cytoplasmic (By similarity).
8 (By similarity).

Extracellular (By similarity).
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Interpro; IPR001140; ABC TWA transpt.
Interpro; IPR005292; MRP_assoc.
Interpro; IPR005292; MRP_assoc.
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965 GYWLSLW 971
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Jupoproterius.";
Jument. Genet. 46:699-705(2001).
Jument. Genet. 46:699-705(2001).
Fulw. Genet. 46:699-705(2001).
Fulw. Genet. 46:699-705(2001).
Fulw. Genet. 40:690-705(2001).
Indirectly. Transports glutathione conjugates as Leukotriene-c4 (ITC4) and N-ethylmaleimide S-glutathione (NEM-GS).
SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
FISSUE SPRCIFICITY: Sapressed in Kidney and liver. Very low expression in other tissues.
DISEASE: Defects in ABCC6 are a cause of autosomal dominant pseudoxanthoma alasticum (AD-PSE) [MIMI-77850]. PXE is a disorder characterized by calcification of elastic fibers in skin, arteries and retina that results in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency and retinal hemorrhages leading to macular degeneration.
DISEASE: Defects in ABCC6 are a cause of autosomal recessive pseudoxanthoma elasticum (AR-PSE) [MIM:264800].
SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
CAUTION: Ref. 2 sequence differs from that shown due to erroneous generation.

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                                                                                                                                                                                                                                 VARIANTS PXE LYS-411; GLN-518; SER-568; PRO-673; GLN-765; PRO-1114; TRP-1121; PRO-1138; GLN-1138; ASP-1203; PHE-1298; ILE-1301, ARG-1302; PRO-1303; GLN-1314; RRP-1321; CYS-1339; HIS-1347; ASN-1361 AND THR-1424, AND VARIANTS ASP-61; ARG-207; GLY-265; GLU-281; VAL-319; LYS-497; ALA-614; GLN-632; HIS-953; CYS-1241 AND GLN-1268. MEDLINE=21426347; PubMed=11536079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATABASE: NAME-Mutations of the ABCC6 gene;
NOTE-Retina International's Scientific Newsletter;
WWW="http://www.retina-international.com/sci-news/abcc6mut.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21558431; PubMed=11702217; DOI=10.1007/s004390100582; Pulkkinen L., Nakano A., Ringpfeil F., Uitto J.; "Identification of ABCCG pseudogenes on human chromosome 16p: implications for mutation detection in pseudoxanthoma elasticum."; Hum. Genet. 109:356-365(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS PXE 60-ARG--TYR-62 DEL; ARG-364 AND ARG-1354, AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                        Le Saux O., Beck K., Sachsinger C., Silvestri C., Treiber C., Goering H.H.H., Johnson B.W., De Paepe A., Pope F.M., Pasquali-Ronchetti I., Bercovitch L., Terry S., Boyd C.D.;
A spectrum of ABCC6 mutations is responsible for pseudoxanthoma
                                                                 VARIANT PXE TRP-1138, AND VARIANT GLN-1268.
MEDLINE=20283940; PubMed=10811882; DOI=10.1073/pnas.100041297;
Ringpfeil F., Lebwohl M.G., Christiano A.M., Uitto J.;
Pseudoxanthoma elasticum: mutations in the MRP6 gene encoding transmembrane ATP-binding cassette (ABC) transporter.";
Proc. Natl. Acad. Sci. U.S.A. 97:6001-6006(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS ALA-614; GLN-632 AND GLN-1268.
MEDLINE-21632166; PubMed=11776382;
Wang J., Near S., Young K., Connelly P.W., Hegele R.A.;
"ABCC gene polymorphism associated with variation in plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am. J. Hum. Genet. 69:749-764(2001).
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EMBL, U91318; AAC15785.1; ALT_SEQ.
EMBL, AF168791; AAD51293.1; -.
HSSP; P08716; IMTO.
Genew; HGNC:57; ABCC6.
  elasticum.";
Nat. Genet. 25:223-227(2000)
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J. Hum. Genet. '
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STRAIN=V583 / ATCC 700802;
STRAIN=V583 / ATCC 700802;
MEDLINE=225508657; PubMed=12663927; DOI=10.1126/science.1080613;
Paulsen I.T., Banerjel L., Myers G.S.A., Nolson K.E., Seshadri R., Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F., Tettellin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R., Nolson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OrderedicousNames=EB73185,
Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                       Gaps
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                                                        Score 42; DB 1; Length 1503;
Pred. No. 6e+02;
2; Mismatches 0; Indels
9 (By similarity).
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                                                            75.0%;
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SEQUENCE FROM N.A.
STRAINS-ATCC 35092 / DSM 1617 / P2;
STRAINS-ATCC 35092 / DSM 1617 / P2;
STRAINS-ATCC 35092 / DSM 1617 / P2;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I.J. Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.D., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gassterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., van der Oost J.;
The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                              MEDINE-20479972; PubMed-11029001; Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                            Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.2%; Score 41; DB 2; Length 413; 62.5%; Pred. No. 2.5e+02; ive 2; Mismatches 1; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update) U-CCT-2003 (TrEMBLrel. 25, Last annotation update) Transport protein relad protein.
OrderedLocusNames=Ta0692;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    acidophilum.";
Nature 407:508-513 (2000).
BMBL; AL45065; CAC11830.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
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GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub. transporter.
Pfam; PF00083; Sugar_tr; I.
PROSITE; PS50850; MFS; 1.
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Best Local Similarity 62.30,
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PROSITE; PS50850; MFS; 1.
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354 GFWETLWG 361
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SEQUENCE 419 AA
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                                                                                                                                                                                                                    NCBI_TaxID=2303;
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A Goffard M., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Goffard M., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blackasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Pociter S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., With B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Mincker P., Souciet J.L.;
Mincker P., Souciet J.L.;
Mincker P., Souciet J.L.;
Minture 430:35-44(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similar to sp|P38071 Saccharomyces cerevisiae YBR026c.
ORFNames-YAL10(19624g;
Yarrowia lipolytica (Candida lipolytica).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                               "Role of mobile DNA in the evolution of vancomycin-resistant Enterococcus faccalis.";
Science 299:2071-2074(2003).
EMBL; AS016957; AAO82859.1; -.
                                                                                                                                                                                                                                                                      73.2%; Score 41; DB 2; Length 266; 62.5%; Pred. No. 1.70+02; ative 2; Mismatches 1; Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382129; CAG82338.1; -.
SEQUENCE 376 AA; 41206 MW; E085FF7C32379DCB CRC64;
                                                                                                                                                                                 Complete proteome; Hypothetical protein.
SEQUENCE 266 AA; 28291 MW; CD6E72C4DF555A36 CRC64;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Created)
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85.7%;
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Best Local Similarity
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Q9HKA9

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RESULT 13

Matches

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RESULT 12

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STRAIN=BP-1;

MEDLINE-21225144; PubMed=12240834;

Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

Matanabe A., Indexaki N.,

Matanabe A., Nakazaki N.,

Matanabe A., Nakazaki N.,

Shimpo S., Sugimoto M., Takauchi C., Yamada M., Tabata S.;

"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";

Matanabe S. 9:123-130(2002).

Matanabe S. 1123-130(2002).

Matanabe M., Matanabe M., Tabata S.;

Matanabe S. 1123-130(2002).

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Query Match 73.2%; Score 41; DB 2; Length 419; Best Local Similarity 62.5%; Pred. No. 2.6e+02; Matches 5; Conservative 2; Mismatches 1; Indels
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08DMV4;
08DMV4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Callulose synthase.
Callulose synthase.
Synchococcus elongatus (Thermosynechococcus elongatus)
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
111 TaxID=32046;
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GFWETLWG 372
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Best Local S
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08DMV4
AC 08DMV
AC 08DMV
DT 01-MA
DT 01-JU
DB Ccllu
GN Synec
OC Bacte
OC Bacte
OC RRP STRQII
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RR MAKAM
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AAY66213	ABP20316	ABP20318	ABP22613	ABP14381	ABP22611	AAU88395	AAU90462	AAU90463	AAU90535	ADE64384	ADH58622	AAW97529	ABP53933	ABJ04488	ADN64476	AAG95260	AAR14709	AAW12859	AAY91924	
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26	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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AMBESS332 standard; peptide; 10 AA.

A ABPSS332 standard; peptide; 10 AA.

AC ABPSS332 standard; peptide SEQ 1D NO:35.

XX ABPSS332

E VEGTR-3 binding peptide SEQ 1D NO:35.

XX Vaccular endothelial growth factor receptor 3 inhibitor; VEGTR-3;

XX Vaccular endothelial growth factor receptor 3 inhibitor; VEGTR-3;

XX Valnerary; cell surface receptor; cancer; necovasculariastion;

XX Valnerary; cell surface receptor; cancer; necovasculariastion;

XX Valnerary; cell surface receptor; cancer; necovasculariastion;

XX Home sapiens.

XX Home sapiens.

XX WO20257299-A2.

XX YAN-2002; 2002WO-IB000099.

XX Town LUDW-) LUDWIG INST CANCER RES.

XX Alitalo K, Koivunen E, Kubo H;

XX Alitalo K, Koivunen E, Kubo H;

XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, recent and diseases of necovascularization.

XX New isolated peptide that inhibits veger and isolated peptide (I) that binds to and chapted and creating disorders mediated by VEGFR-3.

YX New isolated peptide that inhibits will actor receptor 3 (VEGFR-3).

YX New isolated peptide that inhibits growth factor receptor 3 (VEGFR-3).

YX New isolated peptide that inhibits and can be used in gene therapy.

C inhibits vascular endothelial growth factor receptor 3 (VEGFR-3).

YX The resent invention describes and can be used in gene therapy.

C antidiabutic and wulnerary activities and can be useful for chaptoric and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer; e.g. brain, lung, the cell surface receptor VEGFR-3 such as cancer; e.g. brain, lung, lung, lung, lung, lung.
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spleen, kidney, lymph node, small intestine, blood cells,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGRR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and tracting disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
          pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
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  spleen, kidney, lymph node, small intestine, blood cells
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                                                                                                                                                                                                                                             ABP53931 standard; peptide; 10 AA.
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Best Local Similarity
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                                                                      present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vascular endothelial growth factor receptor 3 inhibitor; VBGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
pancreas, colon, stonach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of encovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 5...7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP53968 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                            75.0%; 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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targeting peptide of the invention

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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phase bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting pictides identified by the method of the invention are useful for treating disease states, such as: cidabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; vixal infection; cardiovascular disease and degenerative disease. The present amino acid sequence represents a
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRASIL; targeting peptide; bacterial infection;
Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
viral infection; cardiovascular disease; degenerative disease.
                  pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential
                                                                                                                                                                                                                                            Gaps
liver, spleen, kidney, lymph node, small intestine, blood cells,
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                    Score 50; DB 5; Length 10; Pred. No. 2.3;
                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stem cell (mesenchymal) targeting peptide 61.
                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ04472 standard; peptide; 9 AA.
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17-JAN-2001; 2001US-00765101.
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                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                  1 CGYWLTIWGC 10
                                                                                                                                                                                                                                                                                                                        1 CGYWXXXWXC 10
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                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                             Sequence 10 AA;
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The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The SRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for cidentifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as: diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardlovascular disease and degenerative disease. The present amino acid sequence represents a targeting peptide of the invention
                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                              BRASIL; targeting peptide; bacterial infection; Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; viral infection; cardiovascular disease; degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential
                                                                                                   Gaps
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                                                                                                 Indels
                                                                  Length
                                                                Score 39.5; DB 5;
Pred. No. 1.7e+06;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                             Stem cell (mesenchymal) targeting peptide 50.
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                                                                                                                                                                                                                                                            ABJ04461 standard; peptide; 9 AA.
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17-JAN-2001; 2001US-00765101.
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                                                               54.9%;
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                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                    6; Conservative
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                                                                                                                                                                     CG-WPSWWGC 9
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Best Local Similarity
                                                                    Query Match
Best Local Similarity
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                                  Sequence 9
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Matches
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BRASIL, targeting peptide; bacterial infection;
Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
viral infection; cardiovascular disease; degenerative disease.
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                                                                                                                                  Molt-4 leukaemia cell line targeting peptide 16.
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                                             ABJ04531 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                   07-SEP-2001; 2001WO-US028124.
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17-JAN-2001; 2001US-00765101.
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                                                                                                       (first entry)
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                                                                                                                                                                                                                                           Unidentified
                                                                                                       24-OCT-2002
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                                                                         ABJ04531;
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   Gaps
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   Indels
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 7
                                                                                                                                                                                                                            Stem cell (mesenchymal) targeting peptide 49.
 Mismatches
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                                                                                                                                    ABJ04460 standard; peptide; 9 AA.
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                                                                                                                                                                                                 (first entry)
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5; Conservative
                             1 CGYWLTIWGC 10
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Best Local Similarity
4, Conserve
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                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                 diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection; cardiovascular disease and degenerative disease. The present amino acid sequence represents a targeting peptide of the invention
The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phages to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as:
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Pred. No. 1.7e+06;
0; Mismatches 2;
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Best Local Similarity
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The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGR-3). (I) and cytostatic, hepatotropic, antiinflammatory, hypotensive, antiidabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for the cell surface receptor VEGR-3 such as cancer, e.g. brain, lung, there, spleen, kidney, lymph node, such as cancer, e.g. brain, lung, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and nock, oesophagus, bone, marrow or blood, and diseases of neovascularistion, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangloms and diabetes. The present sequence represents a specifically claimed VEGR-3 binding peptide from the
                                                                              Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; anglogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                VEGFR-3 binding peptide SEQ ID NO:67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; Page 81; 149pp; English
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                (first entry)
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les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-691521/74.
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                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                        Synthetic
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AAY03715
ID AAY0
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AC AAY0
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Kubo H;

/note= "X is any amino acid"

Location/Qualifiers

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the intervalue intervalue of the feature of the containing periode into peptide-containing targeting vectors for use in clinical positron containing targeting vectors for use in clinical positron (fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol group with a labeling reagent of formula: 18F (CH2)m-CRIR2-(CH2)n-X, or a fluorinated alkene in which at least one of the two double bonded carbon atoms bears at least one leaving group comprising I, Br, Cl, azide, cosylate, mosylate, nosylate, nosylate, insylate, insylate, maleimide CC (optionally substituted by 1-2 alkyl) or 3-sulfomaleimide; R1, R2 = I, CR, azide, tosylate, mesylate, nosylate, triflate, m, COM1, COM1, CM sulfonic acid, tertiary ammine, which is used for Radiolabeling peptide-containing targeting vectors such as proteins, antibodies, and R' = 1-6C alkyl or conferency ammonium, COOR', CONR'2 or COR'; and R' = 1-6C alkyl or conferency menonium, coor antibodies, antibody fragments and receptor-cc targeted peptides for use in routine clinical positron emission conferency of the free thiol groups which are rapidly alkylated at contraining and efficient. The method uses the cunique property of the free thiol groups which are rapidly alkylated at contraining a samples of F-18 labeled peptides used in the method of detecting a
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                                                                                                                                                                    /note= "N-terminal acetylation; optionally has a free or protected thiol group"
                                                  18F radionuclide; targeting vector; positron emission tomography; F-18; radiolabeling; thiol; fluorine-18.
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protected thiol group"
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                                                                                                                                                                                                                              'note= "D-form residue'
            Fluorine-18 (F-18) labeled peptide 2.
                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US018268.
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Matches 4; Conserva
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Score 33; DB 5; Lengtn ';
Pred; No. 1.7e+06;

45.8%;

0; Mismatches

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This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and tusion proteins are useful for pre-targetling methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method
                                                                                                                                                                                                                                                                                                                      /note= "acetylated; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"
                                                                                                                                                                                                         Immunogenic peptide; bi-specific antibody; diagnosis; immune response; diseased tissue identification; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "D-form residue, modified with free amino acid protected amino acid group, chelating agent or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bi-specific antibodies that bind specific target tissue and targeted
                                                                                                                                                                           Immunogenic peptide for bi-specific antibody recognition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metal-chelate complex"
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                                                                              AAY76817 standard; peptide; 8 AA.
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14-OCT-1998;
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Sequence 8 AA

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                                                                                                                                                                                                                                                                                                   Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypetrension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                               Gaps
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                              Indels
Length 8;
DB 3; Le
1.7e+06;
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          100.0%; Prea. ...
45.8%; Score 33; 100.0%; Pred. No.
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                                                                                                                                                                             ABP53965 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                           (first entry)
               Best Local Similarity 100.
Matches 4; Conservative
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(LICN ) LICENTIA LTD.
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in the method of the invention.
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                                       Sequence 8 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Targeting an agent towards a target site in a tissue, by administering in a tissue, a multi-specific antibody or its fragment and a polymer conjugate that binds to the capture arm of the multi-specific antibody.
                                                                                                                                                                                                                                                                                                                                                                                               peptide; multi-specific antibody; polymer conjugate; tumour; photodynamic therapy.
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                  33; DB 5; I
No. 1.7e+06;
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                  Score Pred. 1
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                                                                                                                                                                                                                                      ADG94005 standard; peptide; 8 AA.
                  45.8%;
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                                                                                                                                                                                                                                                                                                                                                                Immunogenic peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating cancer and metabolic diseases by administering a multi-specific antibody having a targeting arm that binds to an antigen and a capture arm that binds to a polymer conjugate comprising a therapeutic agent.
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                                                                  Gaps
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                                                                  Indels
   Length 8;
   DB 7; Le
1.7e+06;
45.8%; Score 33; DB 100.0%; Pred. No. 1.7 ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                        ADL98014 standard; peptide; 8 AA.
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31-JUL-2002; 2002US-00209592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-313738/29.
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Sequence 8 AA;

Debymer conjugate, and administering to the tissue a polymer conjugate confidencing and conjugate to a disease and the popular general pages of the polymer conjugate to a disease of disease or disease or disorder the method is receipted as a confidencial controlled to a disease or disorder chosen from cancer (coephoged), agertic, colonic, creetal, pencientic, many breast, overlan, utilizary bladder, endometrial, certal, pencientic, many breast, overlan, utilizary bladder, endometrial, certal, pencientic, many breast, overlan, utilizary bladder, endometrial, certal, pencientic, many breast, overlan, utilizary bladder, endometrial, certal, pencientic, many breast, overlan, utilizary bladder, endometrial, certal, pencientic, many breast, overlan, utilizary bladder, endometrial, certal, pencientic, many breast, overlan, utilizary bladder, endometrial, certal, pencientic, many defense, endometrial, certal, pencientic, many defense, endometrial, pencientic, many defense, endometrial, pencientic, many defense, endometrial, pencientic, pencie a mycoplasma chosen from Mycoplasma arthritidis, M. hyorhinis, M. orale, M. arginini, Acholeplasma laidlawii, M. salivarum and M. pneumoniae. The cancer is preferably chosen from carcinoembryonic antigen (CEA)-expressing tumour or a CD20-expressing malignancy. The present sequence represents a peptide used in the method of the invention.

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                                                                                                                                                                                                                                                                                                                Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis.
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                                 Indels
 45.8%; Score 33; DB 8; Length 8;
                                                                                                                                                                                                                                                                                  Desmoglein-2 CAR sequence cyclic peptide SEQ ID NO 1090.
                 1.7e+06;
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Pred. No. 4.6e+02;
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                                 0; Mismatches
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                                                                                                                                                                                  ABB46346 standard; peptide; 10 AA.
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                   100.0%;
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RESULT 15

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The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a desmosomal cadherin call adhesion recognition CAR sequence (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polynucleotide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autolimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                                                                    Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
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                                                                                                                                  Desmocollin-1 CAR cyclic peptide 9.
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                  ABB46607 standard; peptide; 10 AA.
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                                                                                          30-JAN-2002 (first entry)
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45.8%; Score 33; DB 5; Length 10; 60.0%; Pred. No. 4.6e+02; Artive 0; Mismatches 4; Indels

Query Match
Best Local Similarity 60.0
Matches 6; Conservative

1 CGYWLTIWGC 10 | | | | | 1 CGYATTADGC 10

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Search completed: December 29, 2004, 21:35:32 Job time : 95.3333 secs

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1649, Ap
119, Appl
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Sequence 12, Appl
Sequence 92, Appl
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                                                                      December 29, 2004, 21:20:27 ; Search time 23.6667 Seconds (without alignments) 28.022 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
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           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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S-08-154-712B-21
S-09-947-925A-21
S-09-315-304B-1649
S-08-250-789A-119
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US-09-535-852-1352

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US-09-311-12-12

US-09-311-14A-374

US-09-108-709-22

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Gapop 10.0 , Gapext 0.5
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Sequence 1352, Application US/09535852
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Sequence 1352, Application US/09535852
Sequence 1352, Application US/09535852
Sequence 1352, Application US/09535852
Sequence 1352, Application US/09/535, BSD
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: US/09/535, 852
CURRENT APPLICATION NUMBER: US/09/535, 852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1352
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1090, Application US/09535852

Sequence 1090, Application US/09535852

Patent No. 663911

GENERAL INFORMATION:

APPLICANT: Blachuk, Orest W.

APPLICANT: Symonds, James M.

TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING

TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING

TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086.407C6

CURRENT APPLICATION NUMBER: US/09/515,852

NUMBER OF SEQ ID NOS: 2009

SOFTWARE PRESENCE: 2001-05-21

NUMBER OF SEQ ID NOS: 2009

SEQ ID NO 1090

LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Cyclicized modulating agent comprising OTHER INFORMATION: desmoglein-2 cell adhesion recognition US-09-535-852-1090
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PCT-US95-00296-12
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US-09-810-552-12
US-09-310-552-12
US-09-315-821-1587
US-09-350-641C-1687
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US-09-520-091-24
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ORGANISM: Artificial Sequence
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: circular
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OTHER INFORMATION: Cyclicized modulating agent comprising
OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1352
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Patent No. 5817750
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pacqualini, Renata
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09079432
Patent No. 5955572
GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
NUMBER OF SEQUENCES: 28
                                                                                                                                  Query Match 45.8%; Score 33; DB 4; Length 10; Best Local Similarity 60.0%; Pred. No. 81; Matches 6; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.7%; Score 30; DB 2; Length 8; 80.0%; Pred. No. 3.8e+05; 1ve 0; Mismatches 1; Indels
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MEDLIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,535
FILING DATE: 28-AUG-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REFERENCE/DOCKET VUMBER: 31,815
REFERENCE/DOCKET VUMBER: 31,815
REFERENCE/DOCKET VUMBER: 31,915
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: CANDON OF REPORT OF REPORT OF REDION OF REGION OF SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 80.0°
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TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Diego
STATE: California
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RESULT 5
US-08-986-234-92
US-08-986-234-92
IS-08-986-234-92
Sequence 92, Application US/08986234
Fatent No. 5981706
GENERAL INFORMATION:
APPLICANT: Wallen, et al.
TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
FILE REPRENCE: UNME-0008-1
CURRENT APPLICATION NUMBER: US/08/986,234
CURRENT APPLICATION NUMBER: US/08/986,234
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 2; Length 8; Pred. No. 3.8e+05; 0; Mismatches 1; Indels
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                 ZIP: 92122

ZIP: 92122

MEDIUM TYPER READABLE FORM:
MEDIUM TYPER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,432
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/520,535
FILING DATE: 28-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1794
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
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TELEPAX: (619) 535-9001
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APPLICANT: Cotropia, Joseph P.

TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane Gly
TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane Gly
TITLE OF INVENTION: Human Monoclonal Antibodies Trust. (HIV-1) and Prognosis Tes
TITLE OF INVENTION: Detecting the Presence and Concentration of Antibodies Inhibiting
TITLE OF INVENTION: Pusion-associated Epitope (GCSGKLIC) in gp-41

FILE REFERENCE: 10586/00406

CURRENT APPLICATION NUMBER: US/09/108,709

CURRENT FILING DATE: 1998-07-01

NUMBER OF SEQ ID NOS: 48

SEC ID NOS: 48

SEC ID NO SEG ID NOS: 48

SEC ID NO SEG ID NOS: 48
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GENERAL INFORMATION:

APPLICANT: De LOUGESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTATION OF ANTIBODIES OF
TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
TITLE OF INVENTION: BUTINATARED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPOR:
TITLE OF INVENTION: CONTAINING THEM
TITLE OF INVENTION: CONTAINING THEM
TITLE OF INVENTION: CONTAINING THEM
TITLE OF INVENTION: CONTAINING THEM
TITLE OF INVENTION: CONTAINING THEM
TITLE OF INVENTION: CONTAINING THEM
TITLE OF INVENTION CONTAINING THEM
CURRENT FILING DATE: 2000-05-23
PRIOR PELLING DATE: 1993-11-22
PRIOR FILING DATE: 1993-11-22
PRIOR FILING DATE: 1993-11-22
PRIOR FILING DATE: 1993-03-06
PRIOR FILING DATE: 1993-03-06
PRIOR FILING DATE: 1993-03-06
PRIOR FILING DATE: 1993-03-06
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NAME/KEY: PEPTIDE
LOCATION: (1)...(10)
OTHER INFORMATION: amino acids 600-609 according to the Gnann
OTHER INFORMATION: numbering system
US-09-108-709-22
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100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Human immunodeficiency virus US-09-790-497A-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 110, Application US/09790497A Patent No. 6649735
                                                                                                                                                                 ; Sequence 22, Application US/09108709; Patent No. 6008044; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
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TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT PERIODES AND THEIR USE IN
TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT PRINCESS FOR DETERMINATION OF ANTIBODIES OF
TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
TITLE OF INVENTION: CONTAINING THEM
FILE REFERENCE: 2752-16
CURRENT APPLICATION NUMBER: 09/576,824
FRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: 09/146,028
PRIOR APPLICATION NUMBER: 09/146,028
PRIOR PILING DATE: 1993-03-08
PRIOR PILING DATE: 1993-03-08
PRIOR PILING DATE: 1993-03-08
PRIOR FILING DATE: 1993-03-08
PRIOR FILING DATE: 1993-03-08
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PRIOR FILING DATE: 1993-03-08
PRIOR FILING DATE: 1993-03-08
PRIOR FILING DATE: 1993-03-08
PRIOR FILING DATE: 1993-03-08
PRIOR FILING DATE: 1993-03-06
NUMBER OF SEQ ID NOS: 600
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APPLICANT: Hermanson, Gary G.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Chesnut, Robert W.
APPLICANT: Ishioka Spression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39563-20022.01
CURRENT APPLICATION WUBBER: US 60/085,751
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: HIV1 ENV 69 (peptide 25.0113)
US-09-311-784A-374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 4; Conservative
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LENGTH: 9
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Best Local Similarity 75.v.
---a 3; Conservative
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CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
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2 VWGC 5
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Gaps
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Indels
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Patent No. 5840865
GENERAL INFORMATION:
GENERAL INFORMATION:
FRANZ, Gerald H.
APPLICANT: Franz, Gerald H.
APPLICANT: Loukeris, Athanasios
TITLE OF INVENTION: Bukaryotic Transposable Element
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                  Sequence 4, Application US/07946237

Patent No. 5348874

GENERAL INFORMATION:

APPLICANT: Bavatis, Charalambos

APPLICANT: Franz, Gerald H

APPLICANT: Loukeris, Athanasios

TITLE OF INVENTION: Eukaryotic Transposable Element

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.3%; Score 29; DB 1; Length 5; 75.0%; Pred. No. 3.8e+05;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/946,237

FILING DATE: 19920914

CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:

NAME: David E. Brook

REFERENCE/DOCKET NUMBER: BTT92-01

TELEPHONE: (617) 861-6240

TELEPHONE: (617) 861-6540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: AMINO ACID
;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 3; Conservative
4; Conservative
                                                                                                                                                                                                                                                                                                                                                          Lexington
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                                 7 IWGC 10
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US-08-530-566-10
                                                                                                                          RESULT 10
US-07-946-237-4
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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Matches
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Sequence 10, Application US/09195726

Sequence 10, Application US/09195726

Sequence 10, Application US/09195726

Sequence 10, Application US/09195726

Sequence 10, Application:

APPLICANT: Savakis, Gerald H.

APPLICANT: Loukeris, Athanasios

TITLE OF INVENTION: Bukaryotic Transposable Element

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CANTERNY APPLICATION DATH:
APPLICATION NUMBER: US/08/530,566
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; DB 2; I
Pred. No. 3.8e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REPERENCE/DOCKET NUMBER: BTT92-01ZA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION UNDERR: US 08/239,765
FILING DATE: 09-MAX-1994
PRIOR APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/530,566
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,765
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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) OTHER INFORMATION: Conserved amino acid sequence of the TC-1 family of transposable CTHER INFORMATION: elements US-08-239-765C-4
                                                                                                                                                                                    Gaps
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Sequence 94, Application US/09069827A
Patent No. 6617114
GENERAL INFORMATION:
APPLICANT: FOWLES, Dana M
KAY, Brian K
FRELINGER, Jeffrey A
HYDE-DENYSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29; DB 4; Length 5;
Pred. No. 3.8e+05;
1; Mismatches 0; Indels
                                                                                                                                        40.3%; Score 29; DB 3; Length 5; 75.0%; Pred. No. 3.8e+05;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08239765C

Patent No. 646928

GENERAL INDORMATION:
APPLICANT: Exakis, Charalambos
APPLICANT: Franz, Gerald H
APPLICANT: Loukeris, Athanasios
TITLE OF INVENTION: Eukaryotic Transposable Element
FILE REFERENCE: 18747/1130
CURRENT APPLICATION NUMBER: US/08/239, 765C
CURRENT PILING DATE: 1992-09-14
PRIOR APPLICATION NUMBER: 07/446,237
PRIOR FILING DATE: 1992-09-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Winth Street N.W., Suite 300
CITY: Washington
                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 75.0
Matches 3; Conservative
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                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-067-755-10
         TYPE: amino acid
                                                                                                                                                                                                                               7 IWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 IWGC 10
                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-08-239-765C-4
                                                                                                                                           Query Match
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Pred. No. 3.86+05;
Orannes 0; Indels
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; Patent No. 6225121
erald H.
; APPLICANT: Kinakis, Athanasios
APPLICANT: Kinakis, Apostolos G.
; TITLE OF INVENTION: Eukaryotic Transposable Element
NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STATE: Massachusetts
; COUNTRY: Lexington
; STATE: Massachusetts
; TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,755
FILING DATE: 27-APR-1998
CLASSIFICATION NUMBER: US/09/067,755
FILING DATE: 20-APR-1998
PRIOR APPLICATION NUMBER: US/09/050,566
PRIOR APPLICATION NUMBER: US/08/530,566
PRIOR APPLICATION NUMBER: US/08/239,765
PRIOR APPLICATION NUMBER: US/08/239,765
PRIOR APPLICATION NUMBER: US/08/239,765
PRIOR APPLICATION NUMBER: US/07/946,237
FILING DATE: 14-SEP-1992
ATPONEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/946,237
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: IMBB92-01ZAZ
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 661-6240
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: IME
TELECOMMUNICATION:
TELEPHONE: (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 75.v
Thea 3; Conservative
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                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-195-726-10
                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 IWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VWGC 5
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Search completed: December 29, 2004, 21:36:45 Job time : 24.6667 secs

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Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM protein

Run on:

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Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGETA:
ITLE REFERENCE: 2896/137084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT APPLICATION NUMBER: US/10/046,922
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 72; DB 13; Length 10; 100.0%; Pred. No. 0.0026; Live 0; Mismatches 0; Indels
US-09-832-723-104
US-09-894-018-80
US-09-994-018-185
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US-0-10-302-311-104
US-10-371-525-374
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US-10-371-655-38837
US-10-182-252A-181
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Sequence 34, Application US/10046922
Publication No. US20020164667A1
GENERAL INFORMATION;
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
                                               ; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
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        Query Match
Best Local S
Matches 10
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Sequence 73, Appl
Sequence 77, Appl
Sequence 68, Appl
Sequence 1090, Appl
Sequence 90, Appl
Sequence 39, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 154, Appl
Sequence 178, Appl
Sequence 178, Appl
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                                                                                                                                            December 29, 2004, 21:36:53; Search time 82 Seconds (without alignments) 43.869 Million cell updates/sec
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                            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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3 US-10-046-922-34
3 US-10-046-922-73
3 US-10-046-922-68
7 US-10-046-922-68
7 US-10-654-578-1352
0S-10-654-578-1352
0S-08-821-739A-90
4 US-10-133-210-69
5 US-10-133-210-69
6 US-10-133-210-69
7 US-10-133-210-69
8 US-10-046-922-36
9 US-10-95-22-36
1 US-08-821-739A-78
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                   US-10-046-922-35
72
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                                             Copyright
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APPLICANT: Alitalo, Kari
APPLICANT: Kolvunen, Erkki
APPLICANT: Kubo, Halime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REPERRNCE: 28966/137084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-654-578-1090

Sequence 1090, Application US/10654578

Sequence 1090, Application US/10654578

Publication No. US20040229811A1

GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Brabara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSMAL CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: USENDES. US/10/654,578

CURRENT APPLICATION NUMBER: US/10/654,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
                                                                                         TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
                                                                                                FILE REFERENCE: 2895/1/37046, 922

CURRENT APPLICATION NUMBER: US/10/046, 922

CURRENT FILING DATE: 2002-01-15

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn version 3.0

SOFTWARE: PatentIn version 3.0

LENGTH: 7

I TYPE: PTT

CREAURE: Peptide

FEATURE: STE

NORGANISM: STE

LOCATION: (4)...(6)

COTHER INFORMATION: X at position 4-6 is any amino acid

US-10-046-922-67
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7;
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45.8%; Score 33; DB 13;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 13;
Pred. No. 1.5e+06;
0; Mismatches 3
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LOCATION: (4)..(6)
OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LUCATION: (8)..(8)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-046-922-68; Sequence 68, Application US/10046922; Publication No. US20020164667A1; GENERAL INFORMATION:
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: peptide
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TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REPERENCE: 28967/37084A
CURRENT PILING DATE: 2002-01-15
CURRENT PILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
TYPE: ...
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Publication No. US20020164667A1

GENERAL INFORMATION:

APPLICANT: Altalo, Kari

APPLICANT: Kojvunen, Erki

APPLICANT: Kojvunen, Erki

APPLICANT: Kubo, Hajime

TITLE OF INVENTION: VEGRR-3 INHIBITOR MATERIALS AND METHODS

FILE REFERENCE: 28967/37084A

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

WINDER OF SEQ ID NOS: 80

SOFTWARR: Patentin version 3.0

SEQ ID NO 73

LENGTH: 10
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Pred. No. 2.5;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(1)
CTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
LOCATION: (10)..(10)
OTHER INFORMATION: X is any amino acid
US-10-046-922-34
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i OTHER INFORMATION: X is any amino acid
US-10-046-922-73
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OTHER INFORMATION: X is any amino acid
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APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.4%;
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ORGANISM: isolated peptide
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches 6; Conserva
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US-10-046-922-73
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Gaps

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Sequence 39, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
    APPLICANT: DeLisi, Charles
; APPLICANT: Belisi, Charles
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Gulukota, Dennis
; APPLICANT: Gulukota, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Weng, Chao
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; TITLE OF INVENTION: WIPPLICANT
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; SOFTWARE: PATENTIN VET: 2.00
; SEQ ID NO 39
; LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-133-210-39
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83.3%; Pred. No. 6.8e+02;
cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.4%; Score 32; DB 8; Length 10; 83.3%; Pred. No. 6.8e+02; ive 0; Mismatches 1; Indels
                          PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-01-25
PRIOR PELING DATE: 1994-01-25
PRIOR APPLICATION NUMBER: 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR PILING DATE: 1993-01-05
PRIOR APPLICATION NUMBER: 08/103,396
PRIOR PLING DATE: 1993-08-06
PRIOR FILING DATE: 1993-03-05
PRIOR FILING DATE: 1993-03-05
PRIOR FILING DATE: 1993-03-05
PRIOR FILING DATE: 1993-03-05
PRIOR FILING DATE: 1993-03-05
PRIOR FILING DATE: 1993-08-07
SOFTWARE: PALCHIN NUMBER: 07/926,666
PRIOR FILING DATE: 1993-08-07
SOFTWARE: PALCHIN VERSION 3.1
SEQ ID NO 90
       APPLICATION NUMBER: 08/347,610
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Publication No. US20030103964A1
GRNERAL INFORMATION:
APPLICANT: Berzofeky, Jay
APPLICANT: Glukota, Kamalakar
APPLICANT: Glukota, Kamalakar
APPLICANT: Vaccaro, Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 83.3
Matches 5; Conservative
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; ORGANISM: Homo sapiens
US-08-821-739A-90
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Matches 5; Conser
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US-10-133-210-39
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US-10-133-210-69
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                                                                                                                                                                                                      OTHER INFORMATION: Cyclicized modulating agent comprising OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
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Publication No. US20040229811A1

GENERAL INFORMATION:

APPLICANT: Blachuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING

TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086.407C10

CURRENT APPLICATION NUMBER: US/10/654,578

CURRENT APPLICATION NUMBER: US/10/654,578

CURRENT PILING DATE: 2003-09-03

NUMBER OF SEQ ID NOS: 2009

SOFTWARE: PASLESEQ for Windows Version 4.0

LEMANTH. 10 1352
                                                                                                                                                                                                                                                                                                  Score 33; DB 17; Length 10;
Pred. No. Se+02;
0; Mismatches 4; Indels
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Sequence 90, Application US/08821739A

Publication No. US20020168374A1

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Sette, Alessandro
APPLICANT: Cells, Esteban
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 206,005000A
CURRENT APPLICATION NUMBER: US/08/821,739A
CURRENT FILING DATE: 1999-03-21
PRIOR APPLICATION NUMBER: 06/13,833

PRIOR PILICATION NUMBER: 1996-03-21
PRIOR PILING DATE: 1996-03-21

PRIOR PILING DATE: 1996-03-22

PRIOR FILING DATE: 1996-03-24

PRIOR FILING DATE: 1996-05-26
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CURRENT FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1090
LENGTH: 10
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Similarity 60.0%;
6; Conservative 0
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                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 6; Conserv
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US-08-821-739A-90
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                                                                                       Length 10;
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GREAL INFORMATION:
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Gret, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
FILE REFERENCE: 2060.00500A
CURRENT APPLICATION NUMBER: US/08/821,739A
CURRENT APPLICATION NUMBER: US/08/821,739A
CURRENT FILING DATE: 1996-03-20
PRIOR APPLICATION NUMBER: 08/589,107
PRIOR APPLICATION NUMBER: 08/451,913
PRIOR PLING DATE: 1996-03-26
PRIOR PLING DATE: 1996-03-26
PRIOR PLING DATE: 1994-10-10
PRIOR PLING DATE: 1993-10-20
PRIOR PLING DATE: 1993-10-20
PRIOR PLING DATE: 1993-10-20
PRIOR PLING DATE: 1993-03-06
PRIOR PLING DATE: 1993-03-06
PRIOR PLING DATE: 1993-03-06
PRIOR PLING DATE: 1993-03-05
PRIOR PLING DATE: 1993-03-05
PRIOR PLING DATE: 1993-03-05
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PRIOR PLING DATE: 1993-03-05
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PRIOR PLING DATE: 1993-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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Patent No. US20020098524A1

GENERAL INFORMATION:
APPLICANT: Batell, David A.
APPLICANT: Chen, Yiyou
APPLICANT: Tijerina, Pilar
ITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
FILE REPERENCE: GGG17-
CURRENT APPLICATION NUMBER: US/09/832,723

CURRENT FILING DATE: 2001-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5e+06;
                                                                                    Score 31; DB 10;
Pred. No. 9.3e+02;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.7%; Score 30; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 78, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
     ; OTHER INFORMATION: in this patent. US-09-572-404B-1454
                                                                                    Query Match 43.1%;
Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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Matches 4; Conserv
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US-09-572-404B-1454
US-09-572-404B-1454
; Sequence 1454, Application US/09572404B
; Sequence 1454, Application No. US20030078374A1
; GENERAL INFORMATION:
    APPLICANT: Proteom Ltd
; TILLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFRENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SEQ ID NO 1454
; LENGTH: 10
APPLICANT: Weng, Zhiping
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
TITLE OF INVENTION: COMPOSITIONS THEREOF
FILE REFERENCE: BU-035AX
GURRENT APPLICATION NUMBER: US/10/133,210
CURRENT PILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 281
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
GRANTH: 10
TYPE: PRT
CORGANISM: Attificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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APPLICANT: Roivunen, Erkki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
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Pred. No. 1.5e+06;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 83.
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ORGANISM: Homo Sapiens
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Best Local Similarity
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US-10-046-922-36
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: peptides screened from a phage display random COTHER INFORMATION: peptide library US-09-832-723-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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41.7%; Score 30; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
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18-99-894-018-80
18-99-894-018-80
18-99-894-018-80
18-98DERAL INFORMATION:
18-9PEICANT: EPIMWINE, Inc.
18-9PEICANT: Chestnut, Robert
18-9PEICANT: Chestnut, Robert
18-9PEICANT: Livingston, Brian
18-9PEICANT: Mewman, Mark
18-9PEICANT: Newman, Mark
18-9PEICANT: Newman, Mark
18-9PEICANT: Newman, Mark
18-9PEICANT: Newman, Mark
18-9PEICANT: Newman, Mark
18-9PEICANT: Newman, Mark
18-9PEICANT: Newman, Mark
18-9PEICANT: Newman, Mark
18-9PEICANT: NOWBER: US/09/894,018
18-9PEICATION NUMBER: PCT/US00/35568
18-9PEICATION NUMBER: PCT/US00/35568
18-PRIOR FILING DATE: 2001-16-22
18-PRIOR FILING DATE: 1999-112-28
18-PRIOR PELING DATE: 2001-04-16
18-PRIOR PELING DATE: 2001-04-16
18-PRIOR PELING DATE: 2001-04-16
18-PRIOR PELING DATE: 2001-04-16
18-PRIOR PELING DATE: 2001-04-16
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18-PRIOR DATE: 2001-04-16
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PRIOR APPLICATION NUMBER: US 60/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 117
SEQ ID NO 104
LENGTH: 9
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                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-894-018-80
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Search completed: December 29, 2004, 22:01:39 Job time : 82 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

December 29, 2004, 21:30:17 ; Search time 19 Seconds (without alignments) 50.640 Million cell updates/sec

US-10-046-922-35 72 1 CGYWLTIWGC 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

1102 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRMADTES

SUMMARIES		glutathione transf	hypothetical prote	u	cytochrome-c oxida	T-cell receptor ga	gut pentapeptide	T-cell rec		Ig heavy c	Ig	T-cell receptor ga	:e1]	cell recept	cokinin V -	y cha:	e)	Ig mu chain J regi	UGA3 leader peptid	T-cell receptor l	T-cell receptor be			etical	receptor	receptor	T-cell receptor be		glucuronosyltran	major fat-globule
SUM	ID	871868	A35556	PT0586	T17075	E41946	JH0253	F41946	S19288	PT0324	PT0289	E49033	F49033	C41946	JS0315	PT0230	PH0923	F33932	\$14943	B53284	PT0629	PT0637	A61068	179564	PT0628	PT0642	PT0722	PT0728	PX0008	B48394
	DB	~	~	~	~	8	~	~	~	~	~	~	~	~	~	~	7	~	4	~	~	~	~	4	~	~	~	~	~	N
	Query Match Length	101	10	7	21	10	S	9	80	σ	10	10	10	10	60	10	10	10	10	4	9	9	9	9	7	7	7	7	7	7
*	Query	33.3	33.3	30.6	30.6	29.5	27.8	27.8	27.8	26.4	26.4	26.4	26.4	26.4	25.0	25.0	25.0	25.0	25.0	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6
	Score	24	24	22	22	21	20	20	20	19	19	19	19	19	18	18	18	18	18	17	17	17	17	17	17	17	17	17	17	17
	Result No.		~	e	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

33.3%; Score 24; DB 2; Length 10;

Query Match

pev-kinin 1 - pena	triacylglycerol li	neuromodulatory pe	neuromodulatory pe	neuromodulatory pe	T-cell receptor be	leucokinin VI - Ma	leucokinin VII - M	leucokinin VIII -	angiotensin-conver	adipokinetic hormo	T-cell receptor be	T-cell receptor be	sperm-activating p	hypotrehalosemic h	hypertrehalosemic
PD0029	S57274	833244	833245	S33246	PT0724	JS0316	JS0317	JS0318	A31570	A24244	PT0634	PT0562	A60522	B33995	208997
7	~	~	N	N	~	~	~	N	~	N	N	~	~	N	C3
7	7	7	7	7	6 0	8	80	œ	œ	0	6	6	6	10	10
23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6
17	17	17	17	17	17	17	17	17	17	17	17	17	. 17	17	11
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1	
glutathione transferase (EC 2.5.1.18) class mu 4 - pi	g (fragment)
N'Attender names: gracaumone o'chamaterae crass mu : C'Species: Sus scrofa domestica (domestic pig) C'Date: 19-Mar-1998 #secnence revision 13-Sep-1998 #text change 09-Jul-2004	ext change 09-Jul-2004
C; Accession: S71868 R; Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.	ı
Biochem. J. 317, 879-884, 1996 A; Title: Characterization of pig liver glutathione S-	transferases using HPLC-electrosp
A;Reference number: S71864; MUID:96332484; PMID:8760377 A;Accession: S71868	7.7
A;Molecule type: protein A;Residues: 1-10 <rou></rou>	
A;Cross-references: UNIPROT:07M3E8 C:Comment: At least five species-independent classes of cytosolic glutathion transferases	of cytosolic glutathion transfere
s mitochondrial form are known.	
C; Function:	
A; Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a parhway. detexification: xemphintics metabolism	of intracellular glutathione to
A; Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism	cilitates their further metabolia
es of damage C; Superfamily: glutathione transferase	
#. Score 24: DB 2:	Length 10:
Similarity 100.0%; Pred. No. 9.9e+02 3; Conservative 0; Mismatches 0	Indels 0; Gaps 0;
Oy 2 GYW 4	
Db 4 GYW 6	
RESULT 2	
hypothetical protein (ODC region) - human	
C;Species: Homo Bapiens (Man) C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993	ext_change 30-Sep-1993
C, Accession: A35556	ר ה אוניז י א א אפאיסלוסשנע י די
Kimoshier, U.A.; Gilder, U.D.; Saulca, M.; Dubeseu, U.; Aimoduvar, N.H.; Duk, U. Biol. Chem. 265, 4884-4895, 1990	
A; Title: ISOldtion and expression of a numbar of the A; Reference number: A35556; MUID:90202959; PMID:23188	e uecaiboxyiase gene. 72
A; Accession: A33333 A; Status prelimnary; not compared with conceptual translation	ranslation
A, Rolectie Type: DNA A, Residues: 1-10 <mos></mos>	
A Change and Contract of TARACI	

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A,Molecule type: protein
A,Residues: 1-5 <UES>
A,Experimental source: gut
C,Comment: This peptide increased basal tone of the circular muscle of the esophagogastral and of the circular muscle of the gastro-intestinal junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: F41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
A)C. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: F41946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rjuesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Anguilla japonica (Japanese eel)
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C.Accession: JH0253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Species: Mus musculus (house mouse)
C,Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
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C;Date: 19-War-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S;9288
R;Martin, J;; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
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                 A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-10 <WHE> C;Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.8%; Score 20; DB 2; Length 5; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indel8
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Pred. No. 2.8e+05;
1; Mismatches 2; Indels
                                                                                                                                               Length 10;
                                                                                                                                             Score 21; DB 2; Le
Pred. No. 2.8e+03;
1; Mismatches 2;
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Similarity 40.0%;
2; Conservative 1
                                                                                                                                             Query Match 29.2%;
Best Local Similarity 40.0%;
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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CAVWV 6
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     A, Accession: E41946
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C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: E41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma get A;Reference number: A41946; MUID:92049316; PMID:1658619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:079912; EMBL:U82688; NID:93603112; PID:93603115; PIDN:AAC622
                                                                                                                                                                                                                                   T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: IT-dul-1992 #sequence_revision 17-dul-1992 #text_change 30-May-1997
C;Accession: PT0586; PT0592
R;Feeney, A.J.
J. Exp. Med. 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MuID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Reaidues: 1-7 «FEB»
Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor
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  Pred. No. 9.9e+02;
0; Mismatches 1;
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Pred. No. 2.8e+05;
1; Mismatches 0;
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Pred. No. 2e+03;
0; Mismatches
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C, Keywords: mitochondrion; oxidoreductase
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     75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
Similarity 75.0
3; Conservative
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Matches 3; Conservative
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T-cell receptor gamma chain (1t.60) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ger
A;Reference number: A41946; MuID:92049316; PMID:1658619
A;Accession: C41946
A;Ketus: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-10 cWHE>
C;Keywords: T-cell receptor
C; Accession: E49033; D49033
R; Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B. Eur., J. Immunol. 21, 2999-3007, 1991
A; Title: Functionally distinct subsets of human gamma/delta T cells.
A; Reference number: A49033; MUID:92083926; PMID:1684157
A; Accession: E49033; MUID:92083926; PMID:1684157
A; Accession: E49033
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)
A; Cross-references: GB:872587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A; Cross-references: GB:872587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A; Status: preliminary
A; Molecule type: DNA
A; Estatus: ceferences: GB:872587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A; Cross-references: GB:872587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A; Cross-references: GB:872587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A; Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)
C; Keywords: T-cell receptor
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C.Species: Homo sapiens
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Pred. No. 5.4e+03;
0; Mismatches 2; Indels
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Pred. No. 5.4e+03;
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Similarity 50.0%;
2; Conservative (
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Jo.Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0289
R;Yamada, M: Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
T. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Reference number: DNA
A;Residues: 1-10 <YAM>A;Residues: 1-10 <YAM>A;Residues: leterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: Pr0324
B;Cacession: Pr0324
B;Cacesion: Proferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: Pr0222; MUID:91108337; PMID:1899102
           Biochem. J. 280, 659-662, 1991
A/IILLe: Chemical modification of serine at the active site of penicillin acylase from
A/Reference number: S19288; MUID:92109664; PMID:1764029
A/Accession: S19288
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C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                            27.8%; Score 20; DB 2; Length 8; 40.0%; Pred. No. 2.8e+05; tive 1; Mismatches 2; Indels
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A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                              A;Status: preliminary
A;Nolecule type: protein
A;Residues: 1-8 <MAR.
A;Cross-references: UNIPROT:Q7M124
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Best Local Similarity 40.vv
Local 2; Conservative
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Best Local Similarity 33.3
Matches 2; Conservative
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C;Species: Leucophaea maderae (Madeira cockroach)
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Dacession: JS0319
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic A;Reference number: JS0315
A;Accession: JS0315
A;Accession: JS0315
A;Residues: 1-8 cHOL>
A;Cross-references: UNIPROT:P19987
C;Comemnt: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act C;Keywords: amidated carboxyl end; (Gly) #status experimental
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2; Indels
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25.0%; Score 18; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 4; Indels
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Best Local Similarity 60.0
Matches 3; Conservative
    2; Conservative
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1 GSGFSSWG 8
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3 ITIFG 7
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Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
NCBI_TaxID=179915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Cytochrome c oxidase subunit I (Fragment).
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 Local Similarity 62.5
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NCBI_TaxID=3996;
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P13270;
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Jatropha.
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QBSHF6;
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Q70957 fuerstia af
Cad45547 fuerstia
Q7m3e8 sus scrofa
Q63hn1 bradypodion
Q63h7 neisseria g
Aas16521 neisseria g
Aas16521 neisseria g
Q63bB lepilemur e
Q95dB lepilemur e
Q94nb microcebus
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Compugen Ltd.
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QBSHF6

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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
"Labaditin, a novel cyclic decapeptide from the latex of Jatropha multifida L. (Euphorbiacea). Isolation and sequence determination by means of two-dimensional NMR.";
FEBS Lett. 256:91-96 (1989).
-!- FUNCTION: Labaditin is an active peptide which inhibits the classical pathway of complement activation in vitro. Activity esems to be based on an interaction with Cl.
-!- PTM: This is a cyclic peptide.
-!- PTM: This is a cyclic peptide.
-!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine for treatment of infected wounds, skins infections and scabies.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Malpighiales, Euphorbiaceae, Crotonoideae, Jatropheae,
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SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;
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01-JAN-1990 (Rel. 13, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Q8SHE7
Q8SHF3
Q8SHF9
Q8SHG6
Q8SHG1
Q8SHH1
Q8SH13
Q8SH13
Q8SH13
Q8SH13
Q8SH13
Q8SH13
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Chloroplast.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bokaryota; Viridiplantae; Streptophyta; Core eudicots; asterids;

Jamids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
                                                                                                                                                                                                                                 Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.; "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae) based on three plastid DNA regions."; Mol. Phylogenet. Evol. 31:277-299(2004).

EMBL, AJ505427; CAD45547.1; -.
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"Characterization of pig liver glutathione S-transferases using HPLC-electrospray-lonization mass spectrometry.";
electrospray-lonization mass spectrometry.";
Pick. S71868, S71868.
GO:0004364; F:glutathione transferase activity; IEA.
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Sus arcofa domestica (domestic pig).

Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.

NCBI_TaxID=9825;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Glutathione transferase (EC 2.5.1.18) class mu 4 (Fragment).
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
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Mitochondrion.
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100.0%; Pred. No. ...
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Best Local Similarity 100.
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Best Local Similarity
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lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
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                 SEQUENCE FROM N.A.
MEDLINE=22169767; PubMed=12182400;
Townsend T., Larson A.;
"Molecular phylogenetics and mitochondrial genomic evolution in the chamaeleonidae (Reptilia, Squamata).";
Mol. Phylogenet. Evol. 23:22-36(2002).
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                                                                                                                                                                                                                                             Townsend T.M., Larson A.L.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF444875, AAL90547.1; -GQ; GO:0005739; C:mitochondrion; IEA.
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Pred. No. 1.8e+03;
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14-WAR-2004 (TrEMBLrel. 27, Li
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Ribosomal protein (Fragment).
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10 AA; 1276 MW;
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Best Local Similarity
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Chloroplast.
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PubMed=15084227;
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                                                                                                               Townsend T., Larson A., "Molecular phylogenetics and mitochondrial genomic evolution in the chamaeleonidae (Reptilia, Squamata)."; Mol. Phylogenet. Evol. 23:22-36(2002).
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Pred. No. 4.8e+03;
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SEQUENCE FROM N.A.
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Townsend T.M., Larson A.L.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF448730; AAL90472.1;
GO; GO:0005739; C:mitochondrion; IEA.
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY386266; AAS16521.1; -.
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MEDLINE=22169767; Pubmed=12182400;
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NCBI_TaxID=179888;
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2 WLSRW 6
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MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                                              Snyder L.A., Davies J.K., Saunders N.J.;
Microarray genomotyping of key experimental strains of Neisseria
"Microarray genomotyping of key experimental strains of Neisseria
genorarboea reveals gene complement diversity and five new neisserial
genes associated with Minimal Mobile Elements.";
BMC Genomics 5:23-23(2004).
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Mammalia, Eutheria, Primates, Strepsirhini, Megaladapidae, Lepilemur.
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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Pred. No. 4.8e+03;
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STRAIN-MS11;
SINGET L.A.S., Davies J.K., Saunders N.J.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY386266; AAS16521.1; --
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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20-MAY-2004 (TrEMBLrel. 27, Created)
20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
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GO; GO:0005739; C:mitochondrion; IEA
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GO; GO:0005739; C:mitochondrion; IEA
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01-DEC-2001 (TrEMBLrel. 19,
05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                   Query Match
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                                                            9 AA;
                    Mitochondrion.
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SEQUENCE 9 AA
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Pastcrini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the leamur family cheirogaleidae (primates)
based on mitochondrial DNA sequences";
Mol. Phylogenet. Evol. 19:45-56(2001).
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MEDIINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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Pastorini J., Forstner M.R., Martin R.D.;
"Phylogenetic relationships among Lemuridae (Primates): evidence from
                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Strepsirhini, Megaladapidae, Lepilemur.
NCBI_TaxID=122230,
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Mammalia; Butheria; Primates; Strepsirhini; Daubentoniidae;
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Pred. No. 1.8e+06;
0; Mismatches 0; Indels
                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                       Lepilemur edwardsi (Milne-Edwards's sportive lemur) Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
EMBL, AF224595; AAP33644.1; -.
GO, GO:0005739; C:mitochondrion; IEA.
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EMBL; AF224641; AAK70615.1; -.
EMBL; AF224642; AAK70619.1; -.
                        9 AA
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57.1%;
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Pastcrini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences";
Mol. Phylogenet. Evol. 19:45-56(2001).
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MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                            Gaps
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Mammalia; Butheria; Primates; Strepsirhini; Cheirogaleidae;
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                                         Score 23.5; DB 2; Length 9;
pred. No. 1.8e+06;
0; Mismatches 0; Indels
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D5C563636B5045A2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
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Last annotation update)
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EMBL; AF224636; AAK70595.1; -.
EMBL; AF224637; AAK70599.1; -.
EMBL; AF224638; AAK70607.1; -.
EMBL; AF224639; AAK70607.1; -.
GO, GO.0005739; Cimitochondrion; IEA.
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Pred. No. 1.8e+06;
0; Mismatches 0;
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Mitochondrion.
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Q94XE6;
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SEQUENCE FROM N.A.
MEDLINE-21184272; PubMed=11286490;
MEDLINE-21184272; PubMed=11286490;
Pastorini J., Martin R.D., Ehreemann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
Mol. Phylogenet. Evol. 19:45-56(2001).
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Pastcrini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
"Molecular phylogeny of the leamur family cheirogaleidae (primates)
based on mitochondrial DNA sequences";
Mol. Phylogenet. Evol. 19:45-56(2001).
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SEQUENCE FROM N.A.
MEDLINE=22631663; PubMed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
MEDILINE=22631663; Pubwed=12719521;
Pastorini J., Thalmann U., Martin R.D.;
"A molecular approach to comparative phylogeography of extant Malagasy
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Mammalia, Eutheria, Primates, Strepsirhini, Cheirogaleidae,
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Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
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DR EMBL; AF224624; AAK70551.1; -.

DR EMBL; AF224625; AAK70551.1; -.

DR EMBL; AF224626; AAK70555.1; -.

REMBL; AF224629; AAK70555.1; -.

REMBL; AF224629; AAK70559.1; -.

REMBL; AF224629; AAK70559.1; -.

ROJ; GO:0005739; C:mitochondrion; IEA.

Mitochondrion.

SEQUENCE 9 AA: 116.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit III (Fragment).
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EMBL; AF224630; AAK70571.1; -.
EMBL; AF224631; AAK70575.1; -.
EMBL; AC0005339; C:mitochondrion; IEA.
Mitochondrion.
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                                                                  NCBI_TaxID=122231;
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MEDLINE=21396409; PubMed=11504862;
MEDLINE=21396409; PubMed=11504862;
Shao R., Campbell N.J., Schmidt B.R., Barker S.C.;
Increased rate of gene rearrangement in the mitochondrial genomes of three orders of hemipteroid insects.";
Mol. Biol. Evol. 18:1828-1832(2001).
EMBL, AR355990; AAK55283.1; -..
GO, GO:0005739; C:mitochondrion; IEA.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
h 32.6%; Score 23.5; DB 2; Length 9; Similarity 57.1%; Pred. No. 1.88+06; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.6%; Score 23.5; DB 2; Length 9; 57.1%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome c oxidase subunit III (Fragment).
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Best Local Similarity 57.1%,
A; Conservative
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       Query Match
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Matches 4; Conserv
                                                                                                       3 YWLTIWG 9
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December 30, 2004, 12:55:07; Search time 69.6226 Seconds (without alignments)
51.525 Million cell updates/sec
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geneseqp1990s:*
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geneseqp2001s:* A Geneseq 23Sep04:* geneseqp20048:* Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Abp53931 VEGFR-3 b Abp53931 VEGFR-3 b Adb53968 VEGFR-3 b Adc87481 Human GPC Adc89638 Cancer-re Aac286074 Fc region Adj50741 Human Esr Adm87650 Human Esr Adm87650 Human Esr Adm87650 Human nor Abb49389 Protein e Abb04861 LDL recep Adp2860 Human Sec Aac31487 Human but Aau91293 Human NOV Aac36093 Fc region Adj50706 Human sec Adc97318 E. faeciu Adj81869 P. carugida a Abb73979 Candida a Abb13004 Protein e Adc97318 E. faeciu Adj81869 P. aerugi Ady94989 Human sec Aac97318 E. faeciu Ady94989 Human sec Abb1081 Human sec Abb1081 Human sec Abc97318 Human sec	
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ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:35. ABP53932 standard; peptide; 10 AA. (first entry) 09-JAN-2003 ABP53932; RESULT 1 ABP53932 ID ABE

WO200257299-A2. Homo sapiens. Synthetic.

17-JAN-2001; 2001US-0262476P. 16-JAN-2002; 2002WO-IB000099. 25-JUL-2002.

(LUDW-) LUDWIG INST CANCER RES. (LICN) LICENTIA LTD. Kubo H; Alitalo K, Koivunen E,

WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 13; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

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Sequence 10 AA;
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                                 ovary,
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                         pancreas, colon, stonach, breast, endometrium, prostate, testicle, ovary skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                     Gaps
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spleen, kidney, lymph node, small intestine, blood cells,
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                                                                                                                                                                                                                                                                               Length 10;
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                                                                                                                                                                                                                                                                                                1 Similarity
10; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiogenesis, lymphangiogenesis, vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; ulnerary; cell surface receptor; cancer; neovascularisation; liver disease; hypottension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.
liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                     Length 10;
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                     DB 5;
0.67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "X is any amino acid"
                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                     Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEGFR-3 binding peptide SEQ ID NO:73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 147; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 5. .7
                                                                                                                                                                                                                                                                                                                                                                                                            ABP53968 standard; peptide; 10 AA.
                                                                                                                                                                                                     75.0%; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2002; 2002WO-IB000099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001US-0262476P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LICENTIA LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-691521/74.
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                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 2 GYWLTIWG
                                                                                                                                                                                                                                                                              2 GYWLTIWG
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ADC99638 standard; peptide; 25 AA.

RESULT 5 ADC99638

ADC99638;

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                            pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of meovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a VEGFR-3 binding peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; GPCR; guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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   spleen, kidney, lymph node, small intestine, blood cells,
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                                                                                                                                                                                                                                                                                                                                                Score 50; DB 5; Length 10;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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Pred. No. 91;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 1934; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC87481 standard; protein; 304 AA
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60.0%;
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-2001; 2001JP-00246789
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                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                   Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binder pairs comprising mixing in a reaction vessel phage expressing biological targets and phage expressing target binders, each having biological targets and phage expressing target binders, each having distinguishable selection markers and selection target and target binder pairs based on the selection markers. The molecules of the invention demonstrate cytostatic activity whilst the method may be useful for realing target and target binder pairs for preparing a composition for treating cancer. Furthermore, the method may be utilised during gene therapy procedures. The current sequence is that of the cancer-related Tiel-binder peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selecting target and target binder pairs for preparing a composition for treating cancer by mixing in a reaction vessel phage expressing biological targets and phage expressing target binders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method of selecting target and target
                                                                                                 cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras; leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1; VEGF-R2; VEGF-R3; PMS-related tyrosine kinase 1; FLK1; KDR; Kinase insert domain protein receptor; EGFR; epidermal growth factor; FGFR1; fibroblast growth factor; Tie-1.
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                                                                                                                                                                                                                                                                                                                                                                                            Blume
                                                                                                                                                                                                                                                                                                                                                                                            Dedova O,
                                                                            Cancer-related Tie-1-binder peptide - SEQ ID 476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 26; SEQ ID NO 476; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fc region binding peptide SEQ ID No 54.
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                                                                                                                                                                                                                                                                                                                                                              (DGIB-) DGI BIOTECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                               24-OCT-2001; 2001US-0345471P.
                                                                                                                                                                                                                                                                                                                                                                                            Brissette R, S, Goldstein N;
                                                                                                                                                                                                                                                                                                24-OCT-2002; 2002WO-US034021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%;
                                             entry)
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Best Local Similarity
Matches 6; Conser
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                                                                                                                                                                                                                                    WO2003035839-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            Prendergast J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 AA;
                                                                                                                                                                                                     Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-2003
                                             01-JAN-2004
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Gaps

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6; Conservative

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Query Match Best Local Similarity

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The invention relates to a method of evaluating sample by providing a soluble serum protein (1), one or more compounds physically associated with (1), and a (1)-binding agent that comprises a peptide that specifically binds to (1), allowing the (1)-binding agent to bind to form a complex including one or more compounds physically associated with (1), separating the complex from one or more components of the sample, and evaluating one or more of the physically associated compounds. The sample compress blood or serum, or is obtained from a biopsy. The sample may also be obtained from a tumour or a region within $5 mm of a tumour. The method is useful for detecting modulators that modulate interaction of serum protein-binding compound and serum protein and for identifying binding ligands for serum protein. The present sequence represents a serum albumin-binding peptide identified using the
                                        Evaluating sample comprising soluble serum protein by forming complex comprising serum protein and physically associated compounds using peptide ligand that specifically binds with proteins, which is separated and evaluated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     respiratory; cytostatic; antiarthritic; antiinflammatory; gastrointestinal; antibacterial; immunosuppressive; antidiabetic; antitheumatic; gene therapy; molecular weight marker; chromosome marker; chromosome tag; genetic fingerprinting; nutritional supplement; cancer; inflammatory condition; arthritis; inflammatory bowel disease; crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides and polypeptides, useful for treating, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang J, Ren F, Xue A,
D, Zhao QA, Wang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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                                                                                                                                             Disclosure; SEQ ID NO 278; 191pp; English
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM87650 standard; protein; 136 AA.
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28-MAR-2002; 2002US-00112944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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, Ghosh MJ, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                        method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGFWPRIWG 12
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  WPI; 2004-082161/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGYWLTIWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NUVE-) NUVELO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADM87432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Ya
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM87650;
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    엄
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                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel isolated polypeptides comprising a sequence that binds an immunoglobulin Fc region. The polypeptides are useful as binding molecules for detecting, isolating or purifying immunoglobulin Fc-region polypeptides present in a solution, e.g. blood, plasma or transgenic milk. The Fc-region binding polypeptides are also useful for regulating or preventing an antibody response, or for increasing the half-life and over all stability of a therapeutic or diagnostic compound that is administered to or enters the circulatory system of an individual. This sequence represents an Fc region binding
Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk; antibody response; half-life; stability; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides, useful as binding molecules for detecting, isolating purifying immunoglobulin Fc-region polypeptides present in a solution, for regulating or preventing an antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                            Potter MD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human serum albumin; HSA; serum; blood; tumour; human.
                                                                                                                                                                                                                                                                                                          Ransohoff TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human serum albumin binding peptide, Seq ID No 278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.9%; Score 46; DB 6; 66.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                            Stochl M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ50741 standard, peptide, 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 76; 152pp; English
                                                                                                                                                                                      18-APR-2002; 2002WO-US012492.
                                                                                                                                                                                                                            18-APR-2001; 2001US-0284534P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-2003; 2003WO-US018896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JUN-2002; 2002US-0388642P
                                                                                                                                                                                                                                                                                                            AC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide of the invention
                                                                                                                                                                                                                                                                                                              Ley
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CGFWPRIWG 12
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                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-201220/19.
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                                                                                                                                                                                                                                                                    (DYAX-) DYAX CORP.
                                                                                                                                                                                                                                                                                                            Wu Q,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 AA;
                                                                                                     W0200286070-A2
                                                             Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-2004
                                                                                                                                             31-OCT-2002
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                                                                                                                                                                                                                                                                                                            Rondon IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ50741;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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RESULT 7 ADJ50741

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The present invention describes an isolated polymiciotics (1): (a) when comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b) comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b) which encodes a polypeptide with biological activity, where the comprising a polypeptide with biological activity, where the polymucleotide hybridises to (1) under erringent hybridisation conditions or has greater than 99% sequence identity with (1). (1) has respiratory, correspondint estimathritic, antimidabletic and antirheumatic antibacterial, immunosuppressive, antidabletic and antirheumatic corresponding polymucleotides encoding chimeric or fusion proteins and the terrologues protein sequences. The polymucleotides can be used to capress recombinant protein for analysis, characterisation or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags to identify chromosomes or to map related gene positions; to compare with endogenous bNA sequences in patients to compare with endogenous bNA sequences in patients for genesic disorders; as probes to hybridise and discover genes, related bNA sequences; as a source of information to derive pCR primers for genesic for genetic disorders for attachment to a gene chip or other sequences in the process of discovering other novel polymucleotides; for selecting and making oligomers for attachment to a gene chip or other corporations and polymetides can also be used as antiritional secures or as a source of carbohydrates. The compositions are useful for promoting better or faster closure of nor-challing wounds, for the generation and respensation of tissues, or healing wounds, for the generation and respensation in dreatment of lung or liver fibrosis, compositions are useful for promoting better or faster closure of nor-challing wounds, for the generation and respensation and respensation and sequence cytokine damage. The present sequence reperfusion i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention. N.B. The sequences for this patent were obtained from the USPTO web site from an equivalent US patent US20040048249Al.
cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft versus host disease.
                                                                                                                                                   The present invention describes an isolated polynucleotide (I): (a)
                                                                                               Example 2; SEQ ID NO 743; 591pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU90545 standard; peptide; 20 AA.
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Best Local Similarity 60.vv,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 CGRWDWLWGC 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 136 AA;
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                          Gaps
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0
Score 46; DB 8; Length 136;
Pred. No. 73;
1; Mismatches 3; Indels
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cancer; treatment; anticancer; cytostatic; gene therapy;

Human normal uterus tissue derived protein 43.

19-JAN-2000 (first entry)

AAY59880;

EST; expressed sequence tag.

DE19817946-A1 Homo sapiens.

Human; uterus;

AAY59880 standard; protein; 129 AA.

AAY59880

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Cytostatic, antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-11ke growth factor-1; IGF-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
                                                                                                      Insulin/insulin-like growth factor receptor-binding peptide #2501
                                                                                                                                                                                                               Synthetic
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18-JUN-2002 (first entry)

(META-) METAGEN GES GENOMFORSCHUNG MBH.

98DE-01017946.

98DE-01017946

L7-APR-1998; 17-APR-1998;

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The invention relates to a method of modulating insulin activity in receptor (IR). A composition containing a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor. (IGF-1) receptor are useful for treating insulin-like growth factor (IGF) sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid sequences of the
                                                                                                                                                                                                                                                                                                                Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumors, comprises using peptides that bind to insulin or insulin-like growth factor receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                   Pillutla R, Brandt J;
Ostergaard S, Mandecki WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 5; Length 20;
Pred. No. 20;
0; Mismatches 4; Indels
                                                                                                                                                                                                   Schaeffer L,
J, Cheng W,
Hsiao K;
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 8-3; 390pp; English.
                                                                                                                                             (DGIB-) DGI BIOTECHNOLOGIES LLC (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.5%;
                                                                       29-MAR-2000; 2000WO-US008528.
                                                                                                          29-MAR-2000; 2000WO-US008528
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                 Beasley J, Blume AJ,
Brissette R, Spetzler
Hansen PH, Ravera M,
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WO200172771-A2
                                  04-OCT-2001.
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                                                                                         New nucleic acid sequences expressed in normal uterine tissues, and derived polypeptides, for treatment of uterine cancer and identification of therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                       This invention describes novel cDNA sequences (A) highly expressed in
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Xu HH;
           Dahl
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           Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.5%; Score 45; DB 2; Length 129; 62.5%; Pred. No. 96; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #35465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R,
Yamamoto R,
             Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU49938 standard; protein; 828 AA.
                                                                                                                                                        Claim 23; Page 138; 154pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-00948933.
25-OCT-2001, 2001US-0342921P.
08-FEB-2002, 2002US-0072851.
06-MAR-2002, 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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             Rosenthal A, Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 CSHWLTVW 39
                                            WPI; 1999-591956/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGYWLTIW 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yersinia pestis.
                                                             N-PSDB; AAZ41339
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Wall D,
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated continued or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological contains a gene product or that has an activity against a biological pathway contains a gene product or that has an activity against a biological pathway in which a proliferation-required gene or the biological contains a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that strains is present in a culture or collection of the which each of the strains is present in a culture or collection of the strains; or (13) identifying proteins or screening for homologous nucleic acids required contains and activity; (and a compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for for cellular proliferation to solate candidate molecules for rational activity and activity is a compound and activity is a compound and activity is a compound and activity is a compound and activity is a compound and activity is a compound and activity is a compound and activity is a compound and activity or activity is a compound and activity or activity or activity or activity or activity or activity or activi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Low density lipoprotein receptor binding protein; signal transduction;
LDL receptor binding protein; LDL receptor signalling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                     isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDL receptor binding protein Na channel brain 3 SEQ ID NO:84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 6; Length 828
Pred. No. 4.6e+02;
1; Mismatches 2; Indels
                                                                                                                           SEQ ID NO 77862; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 828 AA;
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                                                                                                                             Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB04861;
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The present invention relates to an isolated nucleic acid molecule
  The present invention describes a method for detecting a stress that alters a functional interaction of a low density lipoprotein (LDL) recepbor binding procein (I) with an LDL receptor interaction domain (II). The method involves introducing a predetermined stress into a system which provides a stress-biased physical interaction of (I) with a stress-biased physical interaction of (I) where in the absence of the stress, the system provides an unbiased interaction of (I) and (II), where a difference between BI and UI indicates that the stress alters the interaction of (I) and (II), and detecting the stress-biased interaction of (I) and (II), and detecting the stress that alters functional interaction of LDL receptor for detecting a stress that alters functional interaction of LDL receptor interaction domain. The method is useful for detecting and modulating signal transduction through LDL receptors. ABBO4778 to ABBO4909 represent LDL receptor binding proteins which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                           Detecting stress that alters interaction of LDL receptor binding polypeptide with LDL receptor interaction domain, comprises detecting difference in stress-biased and unbiased interaction of peptide and domain in a system.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                            Length 1024;
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                                                                                                                                                                                                                                                                                                                                                         Score 44.5; DB 5;
Pred. No. 6.5e+02;
3; Mismatches 1;
                                                                                                                       Disclosure; Page 148-150; 200pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein SEQ ID #617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP29850 standard; protein; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2002; 2002US-0406576P.
29-AUG-2002; 2002US-04065879P.
29-AUG-2002; 2002US-0406588P.
29-AUG-2002; 2002US-0406688P.
29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406614P.
29-AUG-2002; 2002US-0406640P.
29-AUG-2002; 2002US-0406640P.
                                                                                                                                                                                                                                                                                                                                                           61.8%;
54.5%;
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(TEXA ) UNIV TEXAS SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 54.8
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892 CGHWIETMWDC 902
                                                                                                                                                                                                                                                                                                                                                                                                      1 CGYWL-TIWGC 10
                       Gotthardt M;
                                            WPI; 2002-082855/11.
                                                                                                                                                                                                                                                                                                                                     Sequence 1024 AA;
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                       Herz J,
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New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beaurang PA, Behrens D.
Haishan L, Linnemann T;
nang H;
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Halenbeck RF, Huang MM, Kothakota S, Hais
Pierce K, Wang Y, Wong JGP, Wu G, Zhang
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                                                                                                                                                                                                   2002US-0410962P.
2002US-0411019P.
2002US-0411022P.
2002US-0411023P.
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2002US-041101P.
2002US-0411111P.
2003US-0463700P.
2003US-0463708P.
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2003US-0467203P.
2003US-0467230P.
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2003US-0485223P.
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02-MAY-2003; 2
19-MAY-2003; 2
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09-JUN-2003; 2
09-JUN-2003; 2
29-AUG-2002;
29-AUG-2002;
17-SEP-2002;
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22-MAY-2003;
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                                                                                                                                                                                                                                                                                                                                                                           Human; B7-H1.2 protein; Butryophilin 2/3 protein; transplant rejection; immunological condition; graft-versue-host disease; allergy; asthma; inflammatory bowel disease; sepsis; Alzheimer's disease; atherosclerosis; T-cell mediated inflammation; autoimmune disease; multiple sclerosis; systemic lupus erythematosus; autoimmune demyelination; Grave's disease; sporiasis; autoimmune diabetes; diabetes diabetes diabete; reuropathy; HIV infection; rheumatoid arthritis; human immunodeficiency virus; immunosuppressive; gene therapy; infection; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to B7-H1.2 or Butryophilin 2/3 polypeptides of human B7 polypeptide family and polymucleotides encoding such proteins. Sequences of the invention are useful for treating an immunological conditions (e.g., transplant rejection, graft-versus-host disease, allergy, asthma, inflammatory bowel disease, sepsis), diseases that are caused or exacerbated by T-cell mediated inflammation (e.g., Alzheimer's disease or atherosclerosis), autoimmune disease, sepsis), astemic lupus erythematosus, autoimmune disease, disease, psoriasis, multiple solerosis, autoimmune diabetes, diabetic neuropathy, theumatoid arthritis), bacterial or viral infections such as human immunodeficiency virus (HIV) infection, delayed reconstitution of T-cells, defects in T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Butryophilin 2/3 polypeptide of the human B7 polypeptide for treating an immunological condition e.g. transplant
encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                           Gaps
                                                                                                                                                           ö
                                                                                                                                 Length 149;
                                                                                                                                                         1; Indels
                                                                                                                                Score 44; DB 8; I
Pred. No. 1.5e+02;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                         AAE31487 standard; protein; 166 AA
                                                                                                                      61.1%; Scor.
62.5%; Pred
2; N
                                                                                                                                                                                                                                                                                                                                                     Human butryophilin 2/3 protein.
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19-JAN-2001; 2001US-0262737P.
07-JAN-2002; 2002US-00260617.
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                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                  Query Match
Best Local Similarity 62.5-
5, Conservative
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CHFWLTVW 102
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                                                                                                                                                                                   CGYWLTIW 8
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                                                                                                       Sequence 149 AA;
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cell or accessory cell function or congenital immunodeficiencies. They are also used in gene therapy. The present sequence is human butryophilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated cytoplasmic, nuclear, membrane bound and secreted polypeptides, termed NOVX, useful for treating inflammation, autoimmune disorders, hemophilia, Lesch-Nyhan syndrome, pancreatitis,
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ellerman K;
Patturajan M;
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                                                                                                                                                    Length 166;
                                                                                                                                                  Score 44; DB 6; Length 166
Pred. No. 1.6e+02;
1; Mismatches 2; Indels
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Verney CAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rastelli L, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU91293 standard; protein; 415 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-2000; 2000US-0228228; 30-AUG-2000; 2000US-0228324P. 30-AUG-2000; 2000US-0228324P. 30-AUG-2000; 2000US-022838P. 30-AUG-2000; 2000US-0229185P. 01-SEP-2000; 2000US-0229848P. 01-SEP-2000; 2000US-0229848P. 01-SEP-2000; 2000US-0229848P. 22-JAN-2001; 2001US-026518P. 15-MAR-2001; 2001US-0279196P. 27-MAR-2001; 2001US-0279196P.
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                                                                                                                                                       61.1%;
62.5%;
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Padigaru M,
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                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                              127 YWEVVWGC 134
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                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NOV8 protein.
                                                                                                                                                                                                                                                            3 YWLTIWGC
                          are also used in consensus protein
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                                                                                                       Sequence 166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spytek KA
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                                                                                                                                                                                    Best Loc
Matches
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the invention relates to an isolate of yequally NOVI, 2a, 2b, 3a, 3b, 55, 55, 56, 56, 56, 56, 56, 57, 50, 7 and 8), a variant of NOVX, a mature form, or a variant of the mature form of NOVX. Also included are a polymorlectide encoding NOVX (or its complement), a vector comprising the polymorlectide encoding NOVX (or its complement), a vector comprising the polymorlectide, in a sample using the antibody, determining the presence of NOVX polymorlectide in a sample using a probe with binds to NOVX polymorlectide in a sample using a probe with binds to NOVX polymorlectide, in a sample using a probe with binds to NOVX polymorlectide, identifying a an agent which binds to NOVX (including modulators of NOVX) NOVX, the polymorlectide and the antibody are useful for diagnosing, treating or preventing a NOVX-cassociate selected from cardiomyopathy, atherosclerosis.

CC antibody are useful for diagnosing, treating or preventing a NOVX-cassociated disorder related to cell signal processing and metabolic graft versus host disease, Alzhamer's disease, stroke, Lesch-Nyhan cramplantation, allergies, systemic lupus erythematosus, haenophilia, cramplantation, allergies, systemic lupus erythematosus, haenophilia, cramplantation, allergies, systemic lupus erythematosus, and senophilia, parkinson's disease, Alzhamer's disease, hardonesties, paperceatitis, musculoskeletal disorders, pain, neuropsychiatric disorders, hypertension, wound hashing, obesity, growth and reproductive disorders, hypertension, wound chaling, obesity, growth and reproductive disorders, lung diseases and channocamal mapping, tissue typing, forensic biology), coperated in the specification. NOVX, as vaccines to product and the antibody are useful in screening assays, component (e.g., chromosomal mapping, tissue typing, forensic biology), coperated in a two-hybrid or three-hybrid assay; the antibodies immunospecific for NOVX, as vaccines to retend the antibodies immunospecific sessy, the antibodies immunospecific sessy, and principal ringene, hybrid or three-hyb membrane bound invention relates to an isolated cytoplasmic, nuclear,

Sequence 415 AA;

Gaps . 0 61.1%; Score 44; DB 5; Length 415; 62.5%; Pred. No. 3.5e+02; 1; Indels 2; Mismatches 5; Conservative Query Match Best Local Similarity Matches

| :|||:| 95 CHFWLTVW 102 1 CGYWLTIW 8

ઠે 셤 Search completed: December 30, 2004, 13:07:53 Job time : 72.6226 secs

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Sequence 367, App
Sequence 3, Appli
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                                                                                                                                                        December 30, 2004, 12:59:07; Search time 23.0189 Seconds (without alignments) 28.810 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Compugen Ltd.
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US-09-32-147C-3
US-09-270-767-46926
US-09-792-616-9
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US-09-68-335-16
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Sequence 6945, Application US/09107532A
Sequence 6945, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                 Sequence 84, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFWWARE: Patentin Ver. 2.1
SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Maslham
STATE: Massachusetts
COUNTRY: USA
                  US-09-425-043-4
US-08-836-325-12
US-08-836-325-12
US-09-457-571-11
US-09-457-571-7
US-09-634-920-4
US-09-634-920-4
US-09-814-907A-2
US-09-814-907A-2
US-09-814-907A-2
US-09-814-907A-2
US-09-814-907A-2
US-09-814-907A-2
US-09-814-907A-2
US-09-814-907A-2
US-09-814-907A-2
US-09-814-915-4
US-09-814-751-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%; Score 44.5; DB 4;
54.5%; Pred. No. 1.6e+02;
ive 3; Mismatches 1;
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US-09-443-041A-18
US-09-443-041A-22
                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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RESULT 2
US-09-107-532A-6945
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GENERAL INFORMATION:
APPLICANT: Dib-Hajl, Sulayman
APPLICANT: Dib-Hajl, Sulayman
APPLICANT: Dib-Hajl, Sulayman
APPLICANT: Dib-Hajl, Sulayman
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
TITLE OF INVENTION: MOMBER: US/09/354,147C
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1998-11-20
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 2
LENGTH: 1765
                 Sequence 2, Application US/09354147C Patent No. 6573067
                                                                                                                                                                                                                                                                                                                                                                    1.1 PE: P.T.
ORGANISM: Rattus norvegicus
PEATURE:
NAME/KEY: UNSURE
LOCATION: (FF.)
OTHER
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ORGANISM: Rattus norvegicus
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US-09-354-147C-3
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US-09-562-737-86
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Pred. No. 3.1e+02;
1; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.7%; Score 43; DB 4; Length 492; 85.7%; Pred. No. 1.3e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEC ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

PILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

PILING DATE: 14 MAY 1998

APPLICATION NUMBER: 60/051571

PILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REPERENCE/DOCKET NUMBER: 40,489

REPERENCE/DOCKET NUMBER: 40.489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: misc_feature

! LOCATION: (B) LÖCATION 1...492

; SEQUENCE DESCRIPTION: SEQ ID NO: 6945:

US-09-107-532A-6945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
OPERATING SYSTEM: <Unknown>
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US-09-562-737-86
; Sequence 86, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             TELEPRONE: (781)893-507
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6945:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acid
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LENGTH: 1024
TYBE: PR
ORGANISM: Artificial Sequence
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Best Local Similarity 63.6%;
Matches 7; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Sequence 3, Application US/09354147C

Sequence 3, Application US/09354147C

Sequence 3, Application US/09354147C

GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
APPLICANT: Waxman, Stephen G.
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US

CURRENT APPLICATION NUMBER: US/09/354,147C

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US 60/072,990

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR APPLICATION NUMBER: US 60/109,402

PRIOR PRILING DATE: 1999-01-29

PRIOR PILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIN Ver. 2.1

LENGTH: 1765
                                                                                                                                                                                                                       ä
LOCATION: (652)..(1334)
OTHER INFORMATION: Xaa at position 652 is Leu; Xaa at position 1334 is Asn
OTHER INFORMATION: or Lys. Xaa's result from n's in SEQ ID NO: 1.
                                                                                                                                                                                                                          Gaps
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                                                                                                                                                       Query Match 59.0%; Score 42.5; DB 4; Length 1765; Best Local Similarity 54.5%; Pred. No. 5.1e+02; Matches 6; Conservative 2; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: putative amino acid seq. of rat NaN
US-09-354-147C-3
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RESULT 4

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Sequence 3. Application US/09792616

Pageuence No. 6780587

GENERAL INFORMATION:
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
TITLE OF INVENTION: Pseudoxanthoma Elasticum
TITLE OF INVENTION: Pseudoxanthoma Elasticum
TITLE OF INVENTION WHERE: US/09/792,616
CURRENT APPLICATION NUMBER: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 3.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEGUENCES: 496

CORRESPONDENCE ADDRESS:

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

SOFFWANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT TANDER: ASCIT T
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Pred. No. 5.2e+02;
2; Mismatches 0; Indels
                                                                                                                                                                Length 1498;
                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                        Query Match
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
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Best Local Similarity 71.4%;
Matches 5; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-09-792-616-3
                                  ; ORGANISM: Mus musculus US-09-792-616-9
                                                                                                                                                                                                                                                                                                                                                                                                                960 GYWLSLW 966
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965 GYWLSLW 971
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; TYPE: PRT
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                                                                                                        Sequence 187, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Lisham, Annette
APPLICANT: Lisham, Annette
APPLICANT: Lisham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Occapion of forestry plant develc
TITLE OF INVENTION: 1022
CURRENT PAPLICATION NUMBER: US/09/325,932A
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SEQ ID NOS: 206
SEQ ID NO 187
LENGTH: 161
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Sequence 9, Application US/09792616
Patent No. 6780587
GENERAL INFORMATION:
APPLICANT: VINVERSITY OF Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing TITLE OF INVENTION: Pseudoxanthoma Elasticum
TITLE OF INVENTION: Pseudoxanthoma Elasticum
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TITLE OF INVENTION:
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US-09-270-767-46926
; Sequence 46926, Application US/09270767
; Sequence 46926, Application US/09270767
; GENERAL INFORMATION:
; APPLICATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
; TITLE OF INVENTION: NUMBER: US/09/270,767
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT PILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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; ORGANISM: Drosophila melanogaster
US-09-270-767-46926
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                       RESULT 6
US-09-325-932A-187
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LENGTH: 273
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US-09-792-616-9
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US-09-071-035-406

Sequence 406, Application US/09071035

Sequence 406, Application US/09071035

Patent No. 6448043

GENERAL INFORMATION:

APPLICANT: GIL H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
ZIP: 20850
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: SETLING DATE:
FILING DATE:
APPLICATION NUMBER: S. 36,373
REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMUNICATION INFORMATION:
merrenewer: 74011 3109-84614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 81, Application US/09562737

Sequence 81, Application US/09562737

SERERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: US/09/562,737

CURRENT APPLICATION NUMBER: US/09/562,737

CURRENT APPLICATION NUMBER: US/000-05-01

NUMBER OF SEQ ID NOS: 132

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 81

LENGTH: 1024

TYPE: PRT
                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 406
SEGURENCE CHARACTERISTICS:
LENGTH: 266 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
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                                               200 CGAWLGIW 207
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Sequence 2978, Application US/09540236

Batent No. 6673910

GENERAL INFORMATION:
APPLICAMY: Gary L. Breton et al.
TITLE OF INVENTION: NUCLBIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709.2005-001

CURRENT PAPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3630, Application US/09134000C
; Sequence 3610, Application US/09134000C
; Patent No. 6617156
; General INPORMATION:
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERABEUTICS
; FILE REFERENCE: 032796-032
; CURRENT FILING DATE: 1998-08-13
; FRICH APPLICATION NUMBER: US 60/055,778
; PRIOR PALICATION NUMBER: US 60/055,778
; RIOR APPLICATION NUMBER: US 60/055,778
; RIOR SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.9%; Score 41; DB 4; Length 229; 62.5%; Pred. No. 1.2e+02; ive 2; Mismatches 1; Indels
                   TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 408:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                          408:
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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179 GTWITLWG 186
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J. Sequence 87, Application US/09562737

J. Patent No. 6428967

J. GENERAL INFORMATION:

J. APPLICANT: Herz, Joachim

J. APPLICANT: Gotthardt, Michael

J. TITLE OF INVENTION: LDL Receptor Signaling Pathways

FILE REFERENCE: UTSW0708

J. CURRENT APPLICATION: LDL Receptor Signaling Pathways

CURRENT FILING DATE: 2000-05-01

J. NUMBER OF SEQ ID NOS: 132

J. SOFTWARE: PatentIn Ver. 2.1

J. SEQ ID NO 87

J. LENGTH: 1024

J. TYPE: PRT

J. CRGANISM: Artificial Sequence

FRATURE:

J. OTHER INFORMATION: Sequence

J. OTHER INFORMATION: Sequence

J. OTHER INFORMATION: Sequence
) ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                   Query Match 56.2%; Score 40.5; DB 4; Length 1024; Best Local Similarity 54.5%; Pred. No. 5.8e+02; Matches 6; Conservative 2; Mismatches 2; Indels 1.
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892 CGEWIGTMWDC 902
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892 CGEWIETMWDC 902
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US-09-562-737-87
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Search completed: December 30, 2004, 13:19:20 Job time : 24.0189 secs

Sequence 73, Appl Sequence 19313, A Sequence 19313, A Sequence 19014, Sequence 160191, Sequence 15928, A Sequence 1534, Appl Sequence 2376, Appl Sequence 1337, Appl Sequence 1337, Appl Sequence 10, Appl Sequence 2, Appli Sequence 3, Appli Sequence 9, Appli Sequence 187, Appli Sequence 187, Appli Sequence 3, Appli Sequence 3, Appli Sequence 119, Appli Sequence 114, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Appli Sequence 119, Sequence 119, Sequence 119308, Sequence 204642, Sequence 204642, Sequence 204642, Sequence 204642,

US-10-767-701-54778
US-10-125-869A-73
US-10-136-869A-73
US-10-136-9493-13913
US-10-362-297
US-10-363-13913
US-10-312-585-7816
US-10-2122A-5928
US-10-2122A-5928
US-10-2123A-51533
US-10-212-212A-51533
US-10-212-212A-51533
US-10-210-212-21337
US-10-216-1337
US-10-216-1337
US-10-216-220-187
US-10-218-470-3
US-10-218-220-187
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US-10-218-26-338

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100.0%; Score 72; DB 13; Length 10; 100.0%; Pred. No. 0.0026; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Application US/10046922; Publication No. US20020164667A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 34, Application US/10046922; Publication No. US20020164667A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35
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APPLICANT: Koivunen, Erkki
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  US-10-046-922-34
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Sequence 73, Appl
Sequence 2288, Ap
Sequence 1934, Ap
Sequence 476, App
Sequence 54, Appl
Sequence 54, Appl
Sequence 778, App
Sequence 77862, A
Sequence 84, Appl
Sequence 7862, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Appl
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                                                                                                                                                              December 30, 2004, 13:08:04; Search time 74.5283 Seconds (without alignments) 48.267 Million cell updates/sec
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-046-922-34
US-10-046-922-73
US-10-017-161-2288
US-10-292-798-1934
US-10-292-798-1934
US-10-280-066-476
US-10-137-965-125253
US-10-112-9659-54
US-10-12-928-125253
US-10-112-944-743
US-10-282-122-77862
US-10-282-122-77862
US-10-211-962-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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72
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Match Length
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Perfect score:
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No.
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US-10-425-115-204642 US-10-424-599-240891 US-10-425-115-332065 US-10-424-599-179308

ALIGNMENTS

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Gaps

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TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2288
LENGTH: 304
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Variable amino acid FEATURE:
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LOCATION: (107)
OTHER INFORMATION: Variable amino acid
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LOCATION: (79)..(83)
OTHER INFORMATION: Variable amino acid
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LOCATION: (897..(91)
OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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LOCATION: (21<u>9</u>)
OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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OTHER INFORMATION: Variable amino acid
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ABURATANI, HIROYUKI
                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                NAME/KEY: MOD RES
LOCATION: (73)
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LOCATION: (85)
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LOCATION: (123)
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APPLICANT: Alicalo, Kari
APPLICANT: Rolounen, Erkki
APPLICANT: Kolounen, Erkki
APPLICANT: Kolounen, Erkki
APPLICANT: Kolounen, Erkki
APPLICANT: Wolounen, Erki
APPLICANT: Wolounen, Erki
FILE REFERENCE: 28967/37084A
CURRENT FALLING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
LENGTHARE: Patentin version 3.0
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Pred. No. 2.5;
0; Mismatches 4; Indels
               TITLE OF INVENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS FILE REFREENCE: 2896//37084A.
CURRENT APPLICATION VUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 34
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 54; DB 13; Length 10; 100.0%; Pred. No. 0.72; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (1)...(1)
OTHER INFORMATION: X is any amino acid
NAME/KEY: SITE
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; OTHER INFORMATION: X is any amino acid
US-10-046-922-73
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; OTHER INFORMATION: X is any amino acid
US-10-046-922-34
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OTHER INFORMATION: X is any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-046-922-73
; Sequence 73. Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
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                                                                                                                                                                                           TYPE: PRT
ORGANISM: isolated peptide
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.0
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: peptide library
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Kubo, Hajime
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APPLICANT: Brissette, Renee
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Pred. No. 88;
2; Mismatches 1; Indels 1:
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Pred. No. 13;
1; Mismatches 2; Indels
                                                                                                                                                                                   NAME/KEY: MOD_RES
LOCATION: (210)...(211)
PLOCATION: (210)...(211)
PEATURE:
NOMEMERY: MOD_RES
LOCATION: (219)...(219)
OTHER INFORMATION: Variable amino acid
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
                                   PEATURE:
NAME/KEY: MOD_RES
LOCATION: (178)...(178)
OTHER INFORMATION: Variable amino acid
   OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MOD_RES
LOCATION: (256)..(289)
CHER INFORMATION: Variable amino acid
US-10-292-798-1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-280-066-476, Application US/10280066; Sequence 476, Application No. US20030180718A1; Publication No. US20030180718A1; APPLICANT: Pillutla, Renuka C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Tie1-20C-3-D116
US-10-280-066-476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.0%;
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nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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ORGANISM: Eschericia coli
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Best Local Similarity
Matches 6, Conserva
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Best Local S
Matches 6
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Publication No. US20030235833A1

GENERAL INFORMATION:

APPLICANT: SUMA, WAKIKO

APPLICANT: AKIYAMA, YUTAKA

APPLICANT: ARIAMA, YUTAKA

APPLICANT: ABUBATANI, HIROYUKI

TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

FILE REFERENCE: 084335/166

CURRENT FILING DATE: 2002-11-3

PRIOR APPLICATION NUMBER: 10/017,161

PRIOR APPLICATION NUMBER: 10/017,161

PRIOR PILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 2070

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 1934
                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                          DB 14; Length 304;
                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                      Score 47.5; DB
Pred. No. 88;
2; Mismatches
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (256)..(289)
; OTHER INFORMATION: Variable amino acid
US-10-017-161-2288
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LOCATION: (73)..(73)
OTHER INFORMATION: Variable amino acid
FRATURE:
NAME/KEY: MOD RES
LOCATION: (80)..(83)
OTHER INFORMATION: Variable amino acid
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NAME/KEY: MOD RES
LOCATION: (897.. (91)
OTHER INFORMATION: Variable amino acid
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NAME/KEY: MOD RES
LOCATION: (967. (97)
OTHER INFORMATION: Variable amino acid
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LOCATION: (101)..(101)
OTHER INFORMATION: Variable amino acid
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NAME/KEY: MOD RES
LOCATION: (107)..(107)
OTHER INFORMATION: Variable amino acid
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LOCATION: (118)...(119)
OTHER INFORMATION: Variable amino acid
FEATURE:
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LOCATION: (121)...(121)
OTHER INFORMATION: Variable amino acid
                                                                                                                                                                                   66.0%;
60.0%;
                                                                                                                                                                                                                   Best Local Similarity 60.0
Matches 6; Conservative
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NAME/KEY: MOD RES
LOCATION: (123)..(123)
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US-10-292-798-1934
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us-10-046-922-35.rapb

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LOCATION: (1). T. (136)
OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set fort
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APPLICANT: Tang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jen
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Duntul
APPLICANT: Wang, Duntul
APPLICANT: Wang, Zihwel
APPLICANT: Wang, Zihwel
APPLICANT: Wang, Zihwel
TITLE OF INVENTION: Secreted Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.9%; Score 46; DB 15; Length 17; Best Local Similarity 66.7%; Pred. No. 13; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: immunoglobulin binding polypeptide US-10-462-262-278
                   FILE REFERENCE: 10280-052001
CURRENT APPLICATION NUMBER: US/10/462,262
CURRENT FILING DATE: 2003-06-16
FRIOR APPLICATION NUMBER: US 60/388,642
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 430
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR AFELLATION NUMBER: US 09/7409,725
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-02-03
PRIOR PILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-05-18
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CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 743, Application US/10112944 Publication No. US20040048249A1 GENERAL INFORMATION:
  TITLE OF INVENTION: PROTEIN ANALYSIS
                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 CGFWPRIWG 12
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     TITLE OF INVENTION: Brad with TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REPERBNCE: 38-21(5321)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 125253

LENGTH: 63

TYPEP: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.9%; Score 46; DB 14; Length 17; 66.7%; Pred. No. 13; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_27915C.1.pep
US-10-437-963-125253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wound Jeage Jesus
APPLICANT: Wu, Qi-Long
APPLICANT: Wu, Qi-Long
APPLICANT: Ley, Archur C.
APPLICANT: Stochl, Mark
APPLICANT: Stochl, Mark
APPLICANT: Potter, M. Daniel (decessed)
ITILE OF INVENTION: BINDING MOLECULES FOR FC-REGION
ITILE OF INVENTION: BOLYPEPTIDES
FILE REFERENCE: 3421.1006-001
CURRENT APPLICATION NUMBER: US/10/125,869A
CURRENT PILING DATE: 2001-01-11-19
PRIOR APPLICATION NUMBER: 60/284,534
MINDER FILING DATE: 2001-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Fc region binding polypeptide
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 17
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A APPLICANT: Dawson, Bruce M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 6; Conservative
Zhou, Yihua
Cao, Yongwei
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGYWLTIWGC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 CGHYLKAWGC 46
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:| |||
CGFWPRIWG 12
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  APPLICANT:
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SEQ ID NO 84
LENGTH: 1024
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APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION Identification of Essential Genes in Microorganisms
FILE OF INVENTION INDER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
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PRIOR PILING DATE: 2000-10-29
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PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-03-07
PRIOR PILING DATE: 2001-03-03
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                                                                                                 Score 46; DB 15; Length 136;
Pred. No. 73;
1; Mismatches 3; Indels
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Pred. No. 4.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 77862, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
; OTHER INFORMATION: in Example 2 US-10-112-944-743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Chisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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58.3%;
                                                                                                 Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
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Yamamoto, Robert
Forsyth, R.
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Best Local Similarity
Matches 7; Conserv
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LENGTH: 828
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RESULT 12 US-10-211-962-84

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US-IU-437-963-181150
; Sequence 18150, Application US/10437963
; Publication No. US200401233431
; GENERAL INPORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REPERENCE: 38-21(53221)8
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 181150
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7 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
15 OTHER INFORMATION: Sequence
US-10-211-962-84
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Sequence 84, Application US/10211962
Publication No. US20030082640A1
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REPERENCE: USW0708
CURRENT APPLICATION NUMBER: US/10/211,962
CURRENT FILING DATE: 2002-08-01
PRIOR PRICATION NUMBER: US/09/562,737
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78451C.1.pep
US-10-437-963-181150
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Pred. No. 1.1e+02;
4; Mismatches 0
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i. Sequence 54778. Application US/10767701
i. Publication No. US20040172684A1
j. GENERAL INFORMATION:
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50.0%;
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54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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892 CGHWIETMWDC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGYWL-TIWGC 10
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ORGANISM: Oryza sativa
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19 WWVSVWGC 26
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Best Local Similarity
Matches 4; Conserva
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)8
CURRENT PILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 54778
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.1%; Score 44; DB 16; Length 161; Best Local Similarity 75.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.7%; Score 43; DB 14; Length 13; Best Local Similarity 62.5%; Pred. No. 27; Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-125-869A-73

Sequence 73, Application US/10125869A

Sequence 73, Application US/10125869A

Sequence 73, Application US/10125869A

Sequence 73, Application US/10125869A

SPEDICANT: Rondon, Isaac Jesus

APPLICANT: Rondon, Isaac Jesus

APPLICANT: Ley, Arthur C.

APPLICANT: Rensohoff, Thomas C.

APPLICANT: Ransohoff, Thomas C.

APPLICANT: Ransohoff, Thomas C.

APPLICANT: Ransohoff, Thomas C.

APPLICANT: Ransohoff, Thomas C.

APPLICANT: ROLter, M. Daniel (deceased)

TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION

TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION

TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION

TITLE OF INVENTION: DOLYPEPTIDES

FILE REFERENCE: 3421.1006-001

CURRENT APPLICATION NUMBER: 60/284,534

PRIOR FILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 200

SOFTWARE: FASTESEQ for Windows Version 4.0

SEQ ID NO 73

THOMER OF SEQ ID NOS: 200

LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Fc region binding polypeptide US-10-125-869A-73
                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Clone ID: 14593586.pep
US-10-767-701-54778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 CGYWLKPW 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CGYWLTIW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GYWLTIWG 9
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Search completed: December 30, 2004, 13:50:01 Job time : 75.5283 secs

1 GYWCNVWG 8

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 30, 2004, 12:58:17 ; Search time 11.5094 Seconds (without alignments) 83.598 Million cell updates/sec Run on:

US-10-046-922-35 72 1 CGYWLTIWGC 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	80	ID	Description
	46	63.9	218	7	876385	hypothetical prote
7	45	62.5	828	7	AD0412	~
m	43.5	60.4	1993	0	T30902	_
4	42.5	59.0	1765	~	T42388	sodium channel alp
2	42	58.3	72	7	830980	gene 35 protein -
9	42	58.3	441	7	C95307	probable transport
7	42	58.3	1502	~	T42216	multidrug resistan
æ	41.5	57.6		~	F70439	oxaloacetate decar
6	41	56.9		~	T48166	hypothetical prote
10	41	56.9		~	PC4117	replication protei
11	41	56.9	419	7	E90446	permease [imported
	41	56.9	739	7	T29407	hypothetical prote
13	40.5	56.2	200	~	148108	sodium channel alp
	40.5	56.2	1681	~	A55138	channel
15	•	56.2	1682	~	A45380	-
16	•	56.2	1820	ч	CHEE	channel
17	40.5	56.2	1835	~	154323	-
18	40.5	56.2	1836	~	I64893	channel
19	40.5	56.2	1836	~	JS0648	channel
20	•	56.2	1836	~	151964	channel
21	40.5	56.2	1840	Н	CHRTM1	channel
22	•	56.2	1951	N	800320	sodium channel pro
23	•	56.2	1976	N	156555	channel
24	•	56.2	1977	~	S54771	-
25	•	56.2	1983	~	A60054	channel
26	•	56.2	2005	~	A46269	channel
	•	56.2	2005	N	B25019	channel
28	40.5	56.2	2009	~	A25019	channel
	•	56.2	2016	~	A38195	sodium channel pro

sodium channel pro	Ig heavy chain pre	phenylalanyl-tRNA	probable ABC trans	probable Na+/H+-ex	probable ABC trans	genome polyprotein	probable aldo/keto	D-amino-acid oxida	D-amino-acid oxida	D-amino-acid oxida	D-amino-acid oxida	hypothetical prote	neurexin III beta	neurexin III beta
A33996 .	C34903	F97190	F95406	B71038	C95282	S64740	AH0289	JH0185	OXPGDA	S01340	JX0132	AF1978	A53580	B53580
~ ~	9 (7	~	~	~	~	~	N	-	-	-	-	~	~	~
2019	142	339	359	425	508	2344	298	345	347	347	347	376	392	426
56.2	55.6	55.6	55.6	55.6	55.6	55.6	54.9	54.9	54.9	54.9	54.9	54.2	54.2	54.2
40.5	40	40	40	40	40	40	39.5	39.5	39.5	39.5	39.5	39	39	39
30	35	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1
S76385
hypothetical protein - Synechocystis sp. (strain PCC 6803)
A.Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76385 R:Kaneko, T.: Sato, S.: Kotani, H.: Tanaka, A.: Asamizu, E.: Nakamura, Y.: Mivaiima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
Juna Res. 3, 103-130, 1330 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
B.
A; Reference humber: 5/43/2; MulD:9/0012/1; FMLD:69/02/31 A; Accession: 576385
A, Status: preliminary
A; Molecule type: DNA
A;Redidues: 1-218 «KAN» A:Cross-references: UNIPROT:055705: EMBL:D64000: GB:AB001339: NID:G1001484: PIDN:BAA1023
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;superiamily: probable alkaline phospharase yigo
Query Match 63.9%; Score 46; DB 2; Length 218;
ative 1
Qy 1 CGYWLTIWG 9
Db 73 CGYWYGRWG 81
NESULT 2
ADU412 ATD-Appendent helicase (imported) - Versinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accesson: Aboutz C;Accesson: Aboutz D:Das-thill I ween B W . Thomson N D . Tithall B W . Holden M T G . Drentice M.B.
A. Caracara, A. M.; Chillingworth, T.; Cronin, A.; Davies, R. M.; Davies, P.; Dougan, G.; F.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, F
Nature 41, 724-527, 2001 Armit et Geneme sequence of Yersinia bestis, the causative agent of blague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A,Accession: AD0412
A;Status: preliminary A;Molecule type: DNA
A; Residues: 1-828 <kur></kur>
A;/CDB-references: UNIFRCI:QUEDL4; GD:ALD90044; FLUN:CAC94044.1; FLUSED901340; GGFUG.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C
A,Gene: hrpB
C;Supertamily: ATP-dependent KNA nelicase, Hrpb type

62.5%; Score 45; DB 2; Length 828;

Query Match

```
A; Molecule type: DNA
A; Residues: 1-72 <DON>
A; Cross-references: UNIPROT: Q05245; EMBL: Z18946; NID: g15859; PIDN: CAA79411.1; PID: g15891
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C; Genetics:
A; Gene: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95307
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilots
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-ye: .W.R.A;Residues: 1-ye: .W.R.A;Residues: 1-ye: .W.R.A;Residues: 1-ye: .W.R.A;Residues: 1-ye: .W.R.A;Residues: 1-ye: .W.R.A;Residues: 1-ye: .W.B.A;Residues: UNIPROT:Q92ZT6; GB:AE006469; PIDN:AAK65021.1; PID:g14523451; GSPDB:G3*A;Resperimental source: strain 1021, megaplasmid pSymA;Regalibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Dela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.A;Tele: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T42216

R; Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A; Title: Hepatic expression of multidrug resistance-associated protein-like proteins mair
A; Reference number: Z22081; MUID:98279126; PMID:9614210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T42216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rodiecule type: mRNA
A;Rossiques: 1-1502 - MRIR>
A;Cross-references: UNIPROT:088269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3;A;Experimental source: strain Sprague-Dawley; liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable transport protein SMa0684 [imported] - Sinorhizobium meliloti (strain 1021) maga
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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   A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 441;
                                                                                                                                                                                                                                                  Length 72
                                                                                                                                                                                                                                                                                                               2; Indels
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7
                                                                                                                                                                                                                                               Score 42; DB 2
Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 2
Pred. No. 58;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genome: plasmid
C;Superfamily: L-lysine transport protein
                                                                                                                                                                                                                                               58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.3%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                            5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     57
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                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                         1 CGYWLTIW
                                                                                                                                                                                                                                                                                                                                                                                                               CGMWLPVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: C95307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: SMa0684
                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                               Sodium channel SCAP1 alpha chain - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Accession: T30902
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol. 16, 347-356, 1997
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.
A;Reference number: Z20929; MUID:97238630; PMID:9115644
A;Accession: T30902
A;Accession: T30902
A;Accession: T30902
A;Accession: Draininary; translated from GB/EMBL/DDBJ
A;Accession: Draininary; Aranslated from GB/EMBL/DDBJ
A;Accession: Draininary
A;Residues: 1-1993 aDYE>
A;Cross-references: UNIPROT:P90670; EMBL:U66915; NID:g1842248; PID:g1842249; PIDN:AAC474
C;Superfamily: sodium channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sodium channel alpha chain - rat
C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42388
R;Dib-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.
Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998
A;Title: NaN, a novel voltage-gated Na channel, is expressed preferentially in periphera
A;Reference number: Z22149; MUID:98338024; PMID:9671787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1765 CDIB>
A;Cross-references: UNIPROT:O88457; EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC4
A;Experimental source: strain Sprague-Dawley; dorsal root ganglia
A;Note: preferentially expressed in sensory neurons within dorsal root ganglia and trige
C;Superfamily: sodium channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
310980
gene 35 protein - Mycobacterium phage L5
G;Species: Mycobacterium phage L5
C;Species: Mycobacterium phage L5
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A;Titles: Superinfection immunity of mycobacteriophage L5: applications for genetic trans A;Reference number: S30949; MUID:93211283; PMID:8459767
                                   1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                   Indels
                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43.5; DB 2;
Pred. No. 1.3e+02;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
   ed. No. 36;
Mismatches
   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.4%;
54.5%;
   58.3%;
                                                                                                                                               372 CGLWLELLSWGC 383
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                         CGYWLTI--WGC 10
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CGEWIESMWGC 952
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CGEWIENMWGC 764
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Best Local Similarity
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Best Local Similarity
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Dermease [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90446
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Yong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Parrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <KUR>
C;Genetics: UNIPROT: Q97VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:GR
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                              replication protein homolog - Pyrococcus sp. (fragment)
NyAlternate names: hypothetical 391 protein
Cispeciaes: Pyrococcus sp.
Cispeciaes: Pyrococcus sp.
Cibate: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 17-May-1996
CiAccession: PC4117
R.Rashid, N.; Morikawa, M.; Imanaka, T.
R.Rashid, N.; Morikawa, M.; Imanaka, T.
A.Reference number: JC4514; MUID:96105215; PMID:8529878
A.Reference number: JC4514; MUID:96105215; PMID:8529878
A.Recession: PC4117
A.Molecule type: DNA
A.Residues: 1-391 «RAS>
A.Cross-references: DDBJ:D50018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C16C8.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C; Accession: T2940.7 T.T.; Gattung, S. Bubmitted to the EMBL Data Library, November 1996 A; Description: The sequence of C. elegans cosmid C16C8. A; Reference number: 220617
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Pred. No. 78;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 391;
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A;Molecule type: DNA
A;Residues: 1-739 <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 2;
Pred. No. 74;
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Local Similarity 85.7%;
les 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: SS02718
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biot
F;540-613/Domain: lipoyl/biotin-binding homology <LPB>
F;579/Binding site: biotin (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Aquifex acolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70439
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
C, Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. Akeference number: A70300; MUID:98136666; PMID:9537320 A;Accession: F70439 A;Accession: F70439 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                   Score 42; DB 2; Length 1502;
Pred. No. 1.7e+02;
2; Mismatches 0; Indels
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Experimental source: cultivar Columbia; BAC clone T1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oxaloacetate decarboxylase alpha chain - Aquifex aeolicus
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A;Introns: 31/3; 66/2; 114/3; 149/2; 232/2; 284/1
A;Note: T1008.150
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Pred. No. 93;
                                                                       58.3%;
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                                     Best Local Similarity 60.0
Matches 6; Conservative
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Matches 5, Conservative
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CSFVVSIWGC 195
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                                                                                                                                                                                                                                                                964 GYWLSLW 970
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Genetics:

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Proc. Natl. Acad. Sci. U.S.A. 89, 4893-4897, 1992
A;Title: Molecular cloning of an atypical voltage-gated sodium channel expressed in humar A;Reference number: A45380; MUID:92279233; PMID:1317577
A;Accession: A45380
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1682 <GEO-A;Cross-references: UNIPROT:Q01118; GB:M91556; NID:g189046; PIDN:AAA59899.1; PID:g189047
A;Experimental source: heart
A;Note: sequence extracted from NCBI backbone (NCBIP:104344)
C;Superfamily: sodium channel protein
C;Superfamily: sodium channel protein
C;Keywords: glycoprotein; membrane protein; phosphoprotein; sodium channel; voltage-gated
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 56.2%; Score 40.5; DB 2; Length 1682; Best Local Similarity 54.5%; Pred. No. 3.1e+02; Matches 6; Conservative 2; Mismatches 2; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                         sodium channel alpha subunit - long-tailed hamster (fragment)

(;Species: Cricetulus longicaudatus (long-tailed hamster)

(;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

(;Accession: 148108

R;Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.

A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster

A;Reference number: 148108

A;Accession: 148108

A;Accession: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-200 <RES>
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A55138
A55138
A55138
Godum channel mNa2.3, voltage-gated - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A55138
B;Felipe, A.; Knittle, T.J.; Doyle, K.L.; Tamkun, M.M.
J. Biol. Chem. 269, 30125-30131, 1994
A;Title: Primary structure and differential expression during development and pregnancy
A;Title: Primary structure and differential expression A;Felipe A;Accession: A55138
A;Accession: A55138
A;Accession: A55138
A;Accession: A55138
A;Accession: A55138
A;Accession: A55138
A;Accession: A55138
A;Cosseries in RNA
A;Residues: 1-1681 *FEL>
A;Cross-references: UNIPROT: Q62467; GB:L36179; NID: G609544; PIDN: AAA66192.1; PID: G806397
C;Superfamily: sodium channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q60464; GB:M87541; NID:g191069; PIDN:AAA36979.1; PID:g553840
C;Genetics:
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                                                                                                                                          Gaps
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                                                                        Query Match 56.9%; Score 41; DB 2; Length 739; Best Local Similarity 60.0%; Pred. No. 1.38+02; Matches 6; Conservative 1; Mismatches 3; Indels
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             C;Superfamily: myeloperoxidase; myeloperoxidase homology
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Best Local Similarity 54.5
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds (without alignments) 62.362 Million cell updates/sec Run on:

US-10-046-922-35 72 1 CGYWLTIWGC 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*			SUMMAKIES	
Result		Query				
No.	Score	Match	Match Length	DB	σι	Description
1	46	63.9	218	٦	32	8
7	45	62.5	828	N	Q8ZB <u>T</u> 4	
٣	45	62.5	853	N	Q8D1A7	yersinia
4	45	62.5	853	N	AAS60566	66 yersini
2	43.5	0	1993	N	P90670	P90670 aplysia cal
9	43	59.7	168	~	О6н022	
7	43	59.7	221	~	Q74JK6	074jk6 lactobacill
80	43		221	N	AAS08923	Aas08923 lactobaci
6	43		. 501	~	Q6C574	Q6c574 yarrowia li
10	43	59.7	646	7	Q8DKD6	
11	43	59.7	733	N	Q8H2N7	
12	43	59.7	1084	~	Q7WY20	07wy20 pseudomonas
13	42.5	59.0	152	7	Q96AC0	Q96ac0 homo sapien
14	•	59.0	159	~	Q6RW13	homo
15		59.0	S	N	Q9NRW9	homo
16	<u>.:</u>	σ	159	N	Q96PL4	Q96pl4 homo sapien
17	•	σ	159	N	AAR25556	'n
18	٠	σ	263	~	Q7YYF1	Q7yyf1 cryptospori
19	42.5	σ	1765	~	088457	
20	42	58.3	72	-	VG35_BPML5	
21	42	8	133	N	Q855 <u>L</u> 3	
22	42	ω.	284	~	Q6MC01	e.
23	42		284	~	CAF23898	σ
	42	58.3	343	N	Q94FS2	ü
25	42	æ	389	~	083151	-
	42	ø	441	~	Q922T6	
27	42	θ.	452	~	Q83G14	Q83g14 tropheryma
28	42	œ	472	-	RBL_NITVU	_
29	42	58.3	473	0	94 <u>0</u> x60	Q9xd76 nitrobacter
30	42	58.3	473	~	Q9XD77	
31	42	58.3	473	N	Q8VQ84	Q8vq84 nitrosospir

Q8t6h2 dictyosteli Q9r1s7 mus musculu Q8s26 rattus norv Q95.55 homo sapien Q6n1z5 homo sapien Q6744 aquifex aeo Q82z85 enterococcu Q9m030 arabidopsis Q65p64 yarrowia li Q65h94 prrxowia li Q81ud8 homo sapien Q97x97 sulfolobus Q97x77 sulfolobus	Aah59368 homo sapi
Q8T6H2 MRP6_MOUSE MRP6_RAT MRP6_HUMAN Q8N1Z5 Q82285 Q92285 Q9M030 Q9M030 Q9M030 Q9M030	AAH59368
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	41
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	45

ALIGNMENTS

		nypounetical grotein arioss. OrderediocusNames=slr0212; Synechocystis sp. (strain PCC 6803). Bacteria; Cyanobacteria; Chroococcales; Synechocystis.		uka T., Miyajima N.,	Jugura N., Impost 2; the genome of the unicellular cyanobacterium Neguence analysis of the Genome of Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb	enome.";	Mocental).		atic	There are no restrictions on its	Usage by and for commercial	entities requires a license agreement (see nttp://www.isb-sib.cn/announce/ or send an email to license@isb-sib.ch).					163 CRC64;	Length 218; 2; Indels 0; Gaps 0;					late)
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PRT;	ed) sequence update) annotation update)	6803) cocca.	. 62	Kotai	me of 03. I	to 92	SUBCELLULAR LOCATION: INTEGRAL MEMDIANE SIMILARITY: Belongs to the deda family.		is copyright. It stitute of Bioinfo	matics Institute. T institutions as long	and this statement is not removed.	reemei b-sib					1 prot					FRT;	Created) Last sequence update)
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5,25	2666								ខូខ			ខម		Z 2			SOW	Query Best Match	ò	g	25,52	1 2 1 2 1 2	

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Bacteriol. 184:4601-4611(2002)
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STRAIN=KIMS / Biovar Mediaevalis;
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Beng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
"Genome sequence of Yersinia pestis KIM.";
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STRAIN-CO-20 / Biovar Orientalis;

MEDLINE-21470413; PubMed=11586360; DOI=10.1038/35097083;

MEDLINE-21470413; PubMed=11586360; DOI=10.1038/35097083;

MEDLINE-21470413; PubMed=11586360; DOI=10.1038/35097083;

Parkhill J., Warn B.W., Thomson N.R., Churcher C.M., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamiln N. Holroyd S., Jagels K., Karlyshev A.V.,

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Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,

"Genome sequence of Yersinia pestis, the causative agent of plague.";

Nature 413:23-527 (2010).
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                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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Enterobacteriaceae; Yersinia.
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GO; GO:0005679; F:ATP-dependent helicase activity; IEA.
GO; GO:0005679; F:Mucleic acid binding; IEA.
InterPro; IPR001410; DEAD.
InterPro; IPR010225; DEAH box HrpB.
InterPro; IPR010225; DEAH box HrpB.
InterPro; IPR010225; DEAH box HrpB.
InterPro; IPR007502; Helicase—Gom.
Pfam; PF04708; HA2; 1.
Pfam; PF04201; Helicase—C; 1.
Pfam; PF0409; HA2; 1.
Pfam; PF0409; HA2; 1.
Pfam; PF0409; DEAD; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62.5%; Score 45; DB 2; Length 828; 58.3%; Pred. No. 2.4e+02; ive 1; Mismatches 2; Indels
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ATP-binding; Complete profeome, Helicase; Hydrolase.
SEQUENCE 828 AA; 91982 MW; 3A11F88835D5E583 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-QCT-2004 (TrEMBLrel. 28, Last annotation update)
Helicase, ATP-dependent.
Name-hrpB; OrderedLocusNames=YP0291, y0794;
  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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STRAIN=91001 / Biovar Mediaevalis;
SONG Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou I Song Y., Tong Z., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R., Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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Local Similarity 58.3%; Pred. No. 2.5e+02;
Los 7; Conservative 1; Mismatches 2; Indels
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Last annotation update)
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    J. Bacteriol. 186:4338-4349(2004).

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                                                  SEQUENCE FROM N.A.
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PubMed=14966310;
                                                                                                                            Hypothetical
SEQUENCE 16
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AAS08923;
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Q74JK6
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                                                                                          01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2004 (TrEMBLrel. 26, Last amotation update)
Sodium channel alpha-subunit SCAP1.
Aplysia californica (California sea hare).
Rukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
Aplysioidea; Aplysiidae; Aplysia.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Premyella diplosiphon (Calothrix PCC 7601).
Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43.5; DB 2; Length 1993;
Pred. No. 8.9e+02;
3; Mismatches 1; Indels 1.
                                                                 PRT; 1993 AA
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                                                                                                                                                                                                                                                                                                   MEDLINE=97238630; PubMed=9115644;
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Local Similarity 54.5%;
hes 6; Conservative
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                                                                PRELIMINARY;
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942 CGEWIESMWGC 952
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Q6H022;
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P90670;
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                             RESULT 5
P90670
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EMBL, AE017203; AAS08923.1; -..
InterPro; IPR004254; HlylIII.
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                                                                                                                                         59.7%; Score 43; DB 2; Length 168; 66.7%; Pred. No. 1.1e+02; ive 2; Mismatches 1; Indels
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TaxID=33959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Stowe-Evans E., Ford J., Kehoe D.M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY548455; AAT41947.1; -
                                                                       al protein.
168 AA; 18932 MW; 1C9DB963D5210332 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            Q74JK6;
05-UIL-2004 (TrEMBLrel. 27, Created)
05-UIL-2004 (TrEMBLrel. 27, Last sequence update)
05-UIL-2004 (TrEMBLrel. 27, Last annotation update)
Hemolysin-like protein.
OrderedLocusNames=LJ1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Hemolysin-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.7%; Score 43; DB 2; L 62.5%; Pred. No. 1.4e+02; iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                           221 AA
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                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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TIGRFAMB; TIGR01065; hlyIII; 1.
                                                                                                                                            Query Match 59.7
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 62.5
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactobacillus johnsonii
                                                                                                                                                                                                                                                                      122 CGYWLSLRG 130
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SORRARRES

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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hyporhetical protein 001138 B05.118.
Name=001138 B05.118;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                     NEDLINE-2225144; PubNed=12240834;

A Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S. Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kahaina K., Kimura T., Kishida Y., Kinika S., Kidura T., Kishida Y., Shimpo S., Sugimoto M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

I "Complete genome structure of the thermophilic cyanobacterium Thermosphachococcus elongatus BP-1.";

I DNA Res. 9:123-130(2002).

R EMBL; AP005372; BAC08475.1; -.

R GO, GO.003824; F:catalytic activity; IEA.

R InterPro; IRR01932; PP2C-1ike.

R Ffan; PP00481; PP2C; 1.

R SWART; SM00312; PP2C; 1.

R SWART; SM00312; PP2C; 1.

R SWART; SM00312; PP2C; 1.

R SWART; SM00312; PP2C; 1.

R SWART; SM00312; PP2C; 1.

R SWART; SM00312; PP2C; 1.
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62.5%; Pred. No. 3.7e+02;
tive 1; Mismatches 2; Indels
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005486; BAC16197.1; -.
                                                                                                                                                                                       OrderedLocusNames=tl10923;
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPró, IPR001658; DUF594.
Pfam, PR04578; DUF594; 1.
Hypothetical protein.
SEQUENCE 733 AA; 82939 MW; E95884DADIDC2AC9 CRC64;
                                                                                             Last sequence update)
Last annotation update)
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les 5; Conservative
                                                       01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=32046;
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                                                                                                                                                                  Tll0923 protein.
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A Dujon B., Sherman D., Fischer G., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Asigle M., Anthousard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Royer B., Fairhead C., Ferry-Dumazet H., Groppi A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T "Genome evolution in yeasts.";
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                                                                                      Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R., Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.; "The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533."; Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

EMBL, AR017203; AAS08923.1; -- SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                                59.7%; Score 43; DB 2; Length 221; 62.5%; Pred. No. 1.4e+02; tive 2; Mismatches 1; Indels
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SEQUENCE 501 AA; 56411 MW; 91F08EF5A63C60FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Chromosome E of strain CLIB99 of Yarrowia lipolytica-
ORFNames-YALIOE20471g;
Yarrowia lipolytica (Candida lipolytica).
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Best Local Similarity 66.7
Matches 6; Conservative
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GFWLLVWG 179
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                                  STRAIN=NCC 533;
PubMed=14966310;
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Q8DKD6
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RESULT 9
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Best Local Similarity
Matches 7; Conserva
                                SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
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ID Q6
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CC -1- SIMILARITY: Contains 1 histidine kinase domain.

DR 6016020; C:nembrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000156; F:KaTP binding; IEA.

GO; GO:000155; F:Wo-component response regulator activity; IEA.

GO; GO:000155; F:Wo-component signal transduction system (p. . .; IEA.)

GO; GO:000155; F:Wo-component signal transduction system (p. . .; IEA.)

GO; GO:000155; F:Wo-component signal transduction system (p. . .; IEA.)

GO; GO:000155; F:Wo-component signal transduction system (p. . .; IEA.)

GO; GO:000156; F:Wo-component signal transduction system (p. . .; IEA.)

GO; GO:000156; F:Wo-component signal transduction system (p. . .; IEA.)

GO; GO:000156; F:Wo-component signal transduction system (p. . .; IEA.)

InterPro; IPR003594; ATPINIA ATPase.

InterPro; IPR001049; Response reg.

InterPro; IPR001049; Response reg.

FEam; PF00512; HisKA; I.

FEAM; PF00512; HisKA; I.

FEAM; PF00512; HisKA; I.

FEAM; FR00039; Response reg; I.

FEAM; FR00039; Response reg; I.

FEAM; FR00034; PAS; I.

BUSMART; SM00349; RES;

BUSMART; SM00349; RAS;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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PROSITE; PS50894; HPT; 1.
PROSITE; PS50110; RESPONSE REGULATORY; 1.
Kinase; Phosphorylation; Sensory transduction; Transferase.
SEQUENCE 1084 AA; 119129 MW; C953FDDZF273BF1B CRC64;
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Pred. No. 6e+02;
0; Mismatches 3; Indels
                                                                                    Last sequence update)
Last annotation update)
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                                PRT; 1084 AA.
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                                                                  Created)
                                                                                                                                                                                 Pseudomonadaceae; Pseudomonas.
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                                                             01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                       Name=rcsC; ORFNames=RL038;
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nes 6; Conservative
                                PRELIMINARY;
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                                                                                                                                                      Pseudomonas aeruginosa
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                                                  Q7WY20;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE 152 AA; 16669 MW; 637C01214175C3C9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Last ann
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Pfam; PF06396; AGTRAP; 1.
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QJORW9;
QJOCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ATRAP.
ATRAP.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-Kidney;
Ye R.D., He R.;
Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF165187; AAF89547.1; -.
Genew; HGNC:13539; AGTRAP.
InterPro; IPROA336; AGTRAP.
Ffam; PF065986; AGTRAP; 1.
SEQUENCE 159 AA; 17518 MW; 7E012C7E79AE6BC5 CRC64;
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2 GYW-LTIWGC 10
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14 GHWLLTTWGC 23
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Q9NRW9
1D Q9NRW
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Search completed: December 30, 2004, 13:16:10 Job time : 94.2641 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
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AAV14752
ADL17115
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AAR12680
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ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnerary; call surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:67 ABP53964 standard; peptide; 7 AA (first entry)

/note= "X is any amino acid" Location/Qualifiers

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16-JAN-2002; 2002WO-IB000099

L7-JAN-2001; 2001US-0262476P.

Ħ; Kubo Alitalo K, Koivunen E, New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 21; Page 81; 149pp; English.

and The present invention describes an isolated peptide (I) that binds to inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive,

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Matches
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antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGR-3 such as cancer, e.g. brain, lung, liver, spleen, kidhey, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemanglomas and diabetes. The present sequence represents a specifically claimed VEGRR-3 binding peptide from the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointeetinal disorder; inflammatory disease; pancreatitis; atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                   84.2%; Score 32; DB 5; Length 7; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Somatostatin analogue peptide 3181.
                                                                                                                                                                                                                                                                                                                              AAY76794 standard; peptide; 7 AA.
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98US-00203389.
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Best Local Similarity 100.
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                                                                                                                                   present invention
                                                                                                                                                                                                                                                       GYWXXXW
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                                                                                                                                                           Sequence 7 AA;
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cr disulphide. At least one building unit is connected via a bridging group to form a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders such as cancers autoimmune diseases, endocrine disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-aurgical pain. It may also be used for diagnosing cancer. The backbone cyclic analogue is used for imaging the existence of metastesses. Sometostatin analogue is used for imaging the existence of metastesses. Sometostatin analogues can be used for the treatment patients with hormone-secreting and hormone-dependent tumours. They reduce diarrhosa through the effect on intestinal secretion. Sometostatin analogues selective to type of seceptors may be used for treatment of non-insulin dependent diabetes mellitus. They are useful for the prevention of atherosclerosis cand restenosis. The analogues are metabolically stable, selective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-terminally modified with Fmoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Backbone cyclised somatostatin analogue PTR 3181.
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57.1%;
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99WO-IL000329,
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP53418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HORN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GELL/)
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Gellerman G;

This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has one building unit containing a nitrogen atom of the peptide backbone connected to a bridging group comprising an amide, thioether, thioester

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                                                                                                            The present invention describes backbone cyclised somatostatin analogues

(I) that incorporates at least one building unit containing one nitrogen

atom of the peptide backbone connected to a bridging group (comprising an amide, thioether, thioester or disulfide) where at least one building unit is connected via the bridging group to form a cyclic structure with a molety selected from the group consisting of a second building unit, the side chain of an amino acid residue of the sequence or the N-terminal amino acid residue. (I) has antiatteriosclerotic, immunosuppressive, cytostatic, antidiabetic, antilnflammatory and analgesic activities, and creatment of anaecostatin receptor ligand. (I) are useful in the treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-associated complications, endocrine disorders, inflammation, gastrointestinal disorders, pancreatitis, post-surgical pain, and gastrointestinal disorders, pancreatitis, post-surgical pain, and the extensis. (I) can also be used in the disgnosis of cancer, by imaging the existence of metastases, it being labeled with a detectable probe.

The present sequence represents a backbone cyclised somatostatin analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "not an N-terminal amino acid, but condensed with to form a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "not a C-terminal amino acid, but condensed with
to form a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                          New backbone cyclized somatostatin analogs are e.g. useful in the treatment of atherosclerosis, autoimmune diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurokinin A antagonist; tachykinin; respiratory disease; asthma; analgesic; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                               81.6%; Score 31; DB 5; I
57.1%; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harbeson SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "D-form residue"
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                                                                                     Example 12; Page 21; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclo[-Tyr-trp-Leu-Arg-Gly-Trp-].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR93713 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Owen TJ, Kudlacz EM, Buck SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RICH ) MERRELL DOW PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-US000296
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                                                                                                                                                                                                                                                                                                                                                     from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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Tyr(1)
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Trp(6)
             WPI; 2002-681319/73.
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYWKVCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR93713;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment
                            New cyclic peptide derivs. - are neurokinin A and tachykinin antagonists useful e.g. for treating asthma or as analgesics.
                                                                                                        The patent describes novel cyclic hexapeptide and octapeptide compounds which are antagonists of neurokinin A and which are useful medically as analgesics and for treating respiratory diseases such as asthma. The present sequence represents a specifically preferred example of the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a somatostatin analogue of the invention. The invention relates to a backbone cyclised somatostatin analogue that has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                      Score 26; DB 2; Length 6;
Pred. No. 1.7e+06;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Somatostatin analogue peptide 3177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 11; Page 61; 82pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAY76792 standard; peptide; 7 AA.
                                                                             Claim 8; Page 69; 82pp; English
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                                                                                                                                                                                                                                        68.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                         Conservative
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WPI; 1995-336695/43
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                         2 YWXXXW
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                                                                                                                                                                                                           Sequence 6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY76792;
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connected to a bridging group comprising an amide, thioether, thioester connected to a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected via a bridging group to form a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders composition containing the analogue may be used for preventing disorders such as cancers, autoimmune diseases, endocrine disorders, diabetic-associated complications, gastrointestinal disorders, inflammatory consequence at the set of diseases, pancreatitis, atherososlerosis, restenosis and post-surgical pain. It may also be used for disquosing cancer. The backbone cyclic analogues can be used for the treatment patients with hormone-secreting cand hormone-dependent tumours. They reduce diarrhoea through the cand hormone-dependent tumours. They reduce diarrhoea through the cinhibition of vasoactive intestinal peptide (VIP) secretion and by direct conflection may be used for treatment of non-insulin dependent diabetes mellitum. They are useful for the prevention of atherosoclerosis and restenosis; The analogues are metabolically stable, selective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatostopin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer; antidiabetic; antiinflammatory; somatostatin receptor ligand; atterosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis; pancreatitis; post-surgical pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 3; Length 7; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Backbone cyclised somatostatin analogue PTR 3177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "D form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gellerman G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    their in-vivo activities and safe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP53416 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                      65.8%;
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99WO-IL000329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Matches 3; Conservative
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(AFAR/) AFARGAN M M.
(GELL/) GELLERMAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 YWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YWKVCW 7
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7 AA;
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15-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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The present invention describes backbone cyclised somatostatin analogues

(I) that incorporates at least one building unit containing one nitrogen

atom of the peptide backbone connected to a bridging group (comprising an

andie, thioether, thioester or disulfide) where at least one building

unit is connected via the bridging group to form a cyclic structure with

a moiety selected from the group consisting of a second building unit,

the side chain of an amino acid residue of the sequence or the N-terminal

amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,

cytostatic, antidiabetic, antiinflammatory and analgesic activities, and

can be used as a somatostatin receptor ligand. (I) are useful in the

treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-

associated complications, endocrine disorders, inflammation,

castrointestinal disorders, pancreatitis, post-surgical pain, and

restenosis. (I) can also be used in the diagnosis of cancer, by imaging

the existence of metastasses, it being labbled with a detectable probe.

The present sequence represents a backbone cyclised somatostatin analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-HIV; Cytostatic; Immunostimulant; Gene Therapy; Vaccine;
HIV TAT protein transduction domain; human; CEMIS; hemagglutinin domain;
AID; activation induced deaminase; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New chimeric protein useful for treating human immunodeficiency virus infection in a subject, comprises protein transduction domain and a cytidine deaminase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                somatostatin analogs are e.g. useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                              New backbone cyclized somatostatin analogs are e.g. userul in treatment of atherosclerosis, autoimmune diseases and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 5; Length 7; Pred. No. 1.7e+06; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wedekind J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AID target hotspot motif peptide, SEQ ID 9.
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                                                                                       Example 12; Page 21; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ38912 standard; peptide; 4 AA.
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21-OCT-2002; 2002US-0419982P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                           from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
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WPI; 2002-681319/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7 AA;
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The present invention relates to chimeric proteins (I) which comprise a protein transduction domain and a deaminase domain. In (I), the protein transduction domain as chosen from poly-arginine, poly-lyaine peptide, third alpha-helix of Antennapedia homeodomain protein, HSV-1 virion protein (VP)22, HIV-1 Vpr and HIV TAT protein. The deaminase domain comprises CEMIS or Activation Induced Deaminase (AID). (I) further comprises an epitope tag which is a hemagglutinin or a polyhistidine tag, and a polypeptide domain that enhances solubility of (I). (I) further comprises a third polypeptide comprising a cytoplasmic localization protein (e.g. chicken muscle pyruvate kinase) or its fragment which chances localization of the chimeric protein to the cytoplasm. (I) is useful for interrupting HIV infectionin with (I) to allow delivery of (I) into the cell, where (I) binds with vif to interrupt HIV infection or at risk for infectivity, for treating a subject with an HIV infection or at risk for infectivity, for treating a subject with an HIV infection or at risk for the administration step is dose-dependent or transient. (I) is also cuseful for treating a subject for hyper-IgM syndrome which involves administering (I) to a subject exhibiting hyper-IgM syndrome, where (I) take the hyper-IgM syndrome. (I) is useful for treating a subject for Blymphocyte cell lymphoma which involves administering (I) to a subject exhibiting Blymphocyte cell lymphoma, where (I) is taken up by Cancerous Blymphocyte cell lymphoma, where (I) is treating a cancer and infectious diseases. The present sequence was used to illustrate the
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Sequence 4 AA;

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63.2%; Score 24; DB 8; Length 4; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indel8
                               3; Conservative
                Local Similarity
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  Query Match
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Gaps

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AAR76079 standard; peptide; 5 AA AAR76079; RESULT 8

(first entry) (revised) 25-MAR-2003 21-NOV-1995

MAb 55.1 heavy chain CDR1

Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin

gb. Mus WO9515382-A1

94WO-GB002610 29-NOV-1994;

08-JUN-1995.

93GB-00024819. 03-DEC-1993; 03-JUN-1994;

(ZENE) ZENECA LTD

Wright AF; Hall SM, Paterson DS, Copley CG, ú Boot Rose MS, E Blakey DC;

WPI; 1995-215262/28

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complementarity determining region; CDR; autoimmune disease;
inflammation; arthritis; lupus erythematosus; multiple sclerosis;
Hashimoto's thyroiditis; diabetes; uvetits; dermatitis; psoriasis;
urticaria; nephrotic syndrome; glomerulonephritis;
thiflammatory bowel disease; ulcerative collitis; Crohn's disease;
Sjogren's syndrome; allergy; asthma: rhinitis; eczema; insulitis;
graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;
               Antigen binding structures containing CDR's recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis
                                                                                                                  An antigen binding structure is based on the CDRs (given in AAR76078-84) of the heavy and light chains of MAb 55.1 (ECACC 93081901), which recognises the colorectal tumor-associated antigen CA55.1. It is optionally humanized and in the form F(ab')2, F(ab)', Fab, Fv, scFv or V-min, and is produced in transgenic animals or plants. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents complementarity determinating region 1 (CDR H1) of the heavy chain of murine anti-CD23 (FCRRII) monoclonal antibody C11 (see also AAY32263). The invention provides altered antibodies, such as chimeric or humanised antibodies, which comprise sufficient of the amino acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell receptor specific antibodies useful for treating e.g. arthritis, diabetes, multiple sclerosis and psoriasis.
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                                                                                                                                                                                                                                                                                 63.2%; Score 24; DB 2; Length 5; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Light chain CDR H1 of mouse anti-CD23 MAb C11.
                                                                                    Claim 2; Page 96; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY32257 standard; peptide; 5 AA.
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                                 antigen - produced by and therapy of cancer.
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render them capable of binding to the CD23 type II molecule expressed on haematopoietic cells. The antibodies are used to block soluble CD23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soluble peptide analyte; unique recognition sequence; URS; protein detection; clinical diagnosis; environmental diagnosis; anvironmental diagnosis; anthora discovery; protein sequencing; pathogen detection; toxin detection; anthrax toxin; small pox toxin; cholera toxin; anthrax toxin; small pox toxin; cholera toxin; darcksed protein detection array; protein expression profile; drug screening; protein characterisation; disease prognosis; pathologic cell profiling; proteome epitope tag; human; proteome.
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01-JUL-2002; 2002US-0393197P.
01-JUL-2002; 2002US-0393221P.
01-JUL-2002; 2002US-0393223P.
01-JUL-2002; 2002US-0393239P.
01-JUL-2002; 2002US-0393235P.
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Claim 60; SEQ ID NO 496; 134pp; English.

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The invention describes a method of detecting proteins in sample. The method comprises: providing a solution of soluble peptide analytes produced by denaturation and/or cleavage of several sample proteins, and produced by denaturation and/or cleavage of several sample proteins, and optionally, labeling the solution with one or more capture agent(s), where each of the capture agent(s), where each of the capture agent(s), where each of the capture agent(s) and the peptide aunique recognition sequence (URS) of a reference protein; and detecting the binding between one or more of the capture agent sample analytes, where the detection of binding between a capture agent and a peptide analyte indicates the presence of the reference protein in the several of sample proteins. Also described are; and method of guantifying proteins in a biological sample; a method of simultaneously detecting several specific proteins in a multi-protein sample. The method of the invention is used in clinical or environmental diagnosis, drug discovery, protein sequencing and for the detection of a pathogen or cof the invention is used in clinical or environmental diagnosis, drug discovery, protein detection array is useful for: quantifying various forms (such as anthrax toxin, small pox toxin, and cholera toxin). A competitors of natural or non-natural ligands for the capture agent, interest; and to study the relationship between a subject protein capturent of study the relationship between a subject protein characterisation, for screening. The expension are useful for drug screening. The capture agents are useful for drug screening. The study protein my all dation of new potential drug targets as the providing treatment modality suggestion begen tagen or the profiling of the providing treatment modality suggestion begen are useful for identifying and/or detecting a security or screening mand transformation. The methods of saying the environment of a security or screening and security and security or screening and security and security and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.2%; Score 24; DB 8; Length 5; llarity 100.0%; Pred. No. 1.7e+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM10201 standard; peptide; 5 AA.
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produced by denaturation and/or cleavage of several sample proteins, and optionally, labeling the collection of peptides by a detectable part; contacting the solution with one or more capture agent(s), where each of the capture agent(s), where each of the capture agent(s), where each of the capture agent(s), where each of the capture agent(s), and detecting a unique recognition sequence (URS) of a reference protein; and detecting the binding between one or more of the capture agent(s) and detecting consattations and the peptide analytes, where the detection of binding between a capture agent and a peptide analyte indicates the presence of the reference protein in the several of sample proteins. Also described are; and a method of general of sequencing several specific proteins in a multi-protein sample. The method of detecting several specific proteins in a multi-protein sample. The method of detecting several specific proteins in a multi-protein sample. To a packaged protein detection array is useful for: quantifying various forms of the invention is used in clinical or environmental diagnosis, drug discovery, protein sequencing and for the detection of a pathogen or toxins (such as anthrax toxin, small pox toxin, and cholera toxin). A packaged protein detection array is useful for: quantifying various forms of packaged protein detection array is useful for: quantifying various forms of packaged protein detection array is useful for: quantifying various forms of packaged protein and validation of natural or synthetic compounds to interest; and to study the relationship between a subject protein expression profile and that subjects response to a foreign compound or drug. The methods of assaying differential protein expression profile and that subjects response to a foreign compound or carecterisation, for screening, making prognosis of disease outcomes and comparate arrangement modality suggestion based on the profiling present or malignant transformation. The methods of susceptibility of lesions to malignant t
                                                                                                                                                                                                                                                                                                                                                                                                         Detecting proteins comprises providing solution of soluble peptide analytes, contacting solution with capture agents capable of interacting with unique recognition sequence of protein and detecting binding between agents and analytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of detecting proteins in sample. The method comprises: providing a solution of soluble peptide analytes
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                                                                                                                                                                                                                                                                                                            Benkovic SJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 60; SEQ ID NO 525; 134pp; English.
                                                                                                                                                                                                                                                                                                         Zhang S,
                                                                     01-JUL-2002; 2002US-0393223F.
01-JUL-2002; 2002US-0393233F.
01-JUL-2002; 2002US-0393280F.
04-DEC-2002; 2002US-0393280F.
13-DEC-2002; 2002US-0430948P.
                             2002US-0393197P.
  2002US-0393137P
                                                                                                                                                                                                                                                                                                         Meng X, Chan JW,
                                                                                                                                                                                                                                                       (ENGE-) ENGENEOS INC.
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                                               01-JUL-2002;
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Gaps .. 0 63.2%; Score 24; DB 8; Length 5; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels 0; Indels 3; Conservative Local Similarity Query Match Matches

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AAR80643 standard; peptide; 6 AA. AAR80643 RESULT 12
AAR80643
ID AAR80
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AC AAR80

ö AAR80638-R80659 are peptides identified using a new method of peptide detection which involves the use of a pre-selected receptor to which the peptides are isolated by screening libraries which may be very large. The dissociation rate of the individual peptides can be obtained as a measure of the amt. of receptor that binds to each isolate as a function of time. The method is used to identify peptides that are potentially useful as vaccines or as therapeutic or disgnostic agents, i.e. able to bind the pre-selected receptor and act as an agonist or antagonist. The new method enables peptides to be isolated without prior to correct PP field.) Identification of phage encoding a substrate for a specific protease - useful for identification of peptide(s) potentially useful as vaccines, therapeutic or diagnostic agents. Gaps vaccine; isolation; diagnosis; receptor; bacteriophage; ö 63.2%; Score 24; DB 2; Length 6; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels Receptor binding peptide used in a new isolation method Dower WJ; Example 3; Col 29; 28pp; English. (AFFY-) AFFYMAX TECHNOLOGIES NV 90US-00541108. 91US-00718577. (revised)
(first entry) 3; Conservative Cwirla SE, oligonucleotide library Local Similarity WPI; 1995-254429/33. 1 GYW 3 Sequence 6 AA; 20-JUN-1991; 20-JUN-1990; 25-MAR-2003 05-MAR-1996 Barrett RW, US5432018-A. 11-JUL-1995 Protease; Synthetic Query Match Matches ð 셤

AAU83934 standard; peptide; 6 AA. 08-MAY-2002 (first entry)

AAU83934

Tyrosine recombinase; antibacterial; cytostatic; cell growth modulator; site-specific DNA recombinase; type I DNA topoisomerase; tumour; tyrosine recombinase; cancer; Holliday junction. Tyrosine recombinase inhibitory peptide #37

Synthetic

27-DEC-2001.

WO200198540-A2

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Stevens AP;
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                                                                                          Disclosure, Fig 1; 39pp; English
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         WPI; 2003-221549/21
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                                                                                                                                                                                                         The method relates to a method of identifying a modulator of cell growth, comprising assessing and comparing the activities of site-specific DNA recombinase (I) or type I DNA topoisomerase (II) in presence and absence of a test substance. A difference in activity of (I) and (II) assessed in the presence and absence of the test substance indicates that the test substance modulates cell growth. The identified cell growth modulator, preferably an inhibitor of (I) or (II), is useful for inhibiting cell growth in a subject, preferably a human. The inhibitor inhibits (I) which is preferably tyrosine recombinase or type I DNA topoisomerase in humans having or suspected of having tumnour or cancer, where the method further involves administering an effective of antitumour or anticancer agent or treatment; or who are, or are suspected of being infected by a bacterium, in which case the inhibitor inhibits Holliday junction intermediate resolution activity of tyrosine recombinase. The method further involves administering an effective amount of antibiotic or antibacterium.
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                                                                                                                             Identifying cell growth modulators for inhibiting cancer cell growth in humans, involves assessing and comparing activity of site-specific recombinase or type I DNA topoisomerase in presence/absence of test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodopsin related G-protein coupled receptor binding site peptide #98
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                                                        (UYSA-) UNIV SAN DIEGO STATE FOUND.
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                                                                                                                                                                                        Claim 39; Page 90; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABJ37222 standard; peptide; 6 AA.
                                 22-JUN-2000; 2000US-00602087.
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         21-JUN-2001; 2001WO-US020046.
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                                                                                Pinilla C;
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                                                                                Segall A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for producing a compound library. The novel method involves reducing a biological target into a group of
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Producing compound library, by generating biological target model using target sequence information, defining microenvironments interacting with ligand and motifs interacting with microenvironment, and assembling
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one or more amino acids required for interaction with a ligand, to generate a model of the biological target, using the model to define a microenvironment in the biological target capable of interacting with the ligand, defining motifs which interact with the microenvironment, and assembling the motifs to generate a compound library for synthesis. The novel method is useful to produce compound libraries for screening natural ligands such as peptides and proteins or for producing cohemical compounds based on drug motifs for screening. This sequence represents a peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin, which relates to the novel compound library production method of the invention 88888888888888888

Sequence 6 AA;

Gaps ô Query Match 63.2%; Score 24; DB 6; Length 6; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 3; Conservative 0; Mismatches 0; Indels

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Sequence 16, Appl
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Sequence 653, App
Sequence 1579, App
Sequence 39, Appl
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Sequence 38, Appl
Patent No. 5185431
Sequence 6, Appli
                                                                                                                   December 29, 2004, 21:56:54; Search time 36 Seconds (without alignments) 12.895 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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US-09-315-304B-653
US-09-315-304B-1579
US-09-350-325-39
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US-07-918-577-6

US-08-443-30

US-08-462-720-30

US-09-38-788-2

US-09-069-827A-94

US-09-653-22C-53

US-08-941-260A-2

US-08-884-569A-11

US-08-884-569A-11

US-08-884-569A-11

US-08-884-569A-11

US-08-484-569A-11

US-08-484-569A-11

US-08-484-569A-11

US-09-743-492A-5

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US-08-991-258A-5

US-08-991-258A-5

US-08-991-258A-5

US-08-991-258A-5

US-08-991-258A-5

US-08-991-953A-5
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US-08-753-750B-3
5185431-15
                                                                                                                                                                                                                                                                                                                            478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                             US-10-046-922-67
38
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Match Length
                                Copyright
                                                                                                                                                                                                                                   1 GYWXXXW 7
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Perfect score:
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Sequence 653, App
Sequence 653, App
Sequence 1579, App
Sequence 1579, App
Sequence 22, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-753-750B-38
Sequence 38, Application US/08753750B
Sequence 38, Application US/08753750B
Sequence 38, Application US/08753750B
SENERAL INFORMATION:
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Society Anthony B.
APPLICANT: Pottery Andrew A.
TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
               US-09-515-965A-653
US-09-150-641C-653
US-09-150-641C-1579
US-09-150-641C-1579
US-08-480-434-31
US-08-053-451B-22
US-08-053-451B-22
US-08-053-451B-31
5217869-14
US-07-718-577-10
US-07-718-577-10
US-07-718-577-10
US-07-918-577-10
US-07-918-577-10
US-07-918-577-10
US-07-918-577-10
US-07-918-577-10
US-08-487-006-67
US-08-487-006-88
US-08-488-659A-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08353400 Patent No. 5665357 GENERAL INFORMATION:
                                                            440000000000000
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Best Local Similarity 100.
Matches 3; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PRONUBER OF SEQUENCES: 3 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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RESULT 5
US-07-973-235A-30
; Sequence 30, Application US/07973235A
; Patent No. 5491130
; GENERAL INFORMATION:
; APPLICANT: David D. Roberts, et al.
; TITLE OF INVENTION: Related Collagen-Binding Proteins
; TITLE OF INVENTION: Related Collagen-Binding Proteins
; TITLE OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STARE: Virginia
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                        FILING DATE: 19910620
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/541,108
FILING DATE: 20-UN-1990
ATTONNEY/AGENT INPORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-25-1
TELECOMUNICATION INPORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-242
INPORMATION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/07/973,235A
FILING DATE: 19921110
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ROBERT L. Price
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER:
TELECHONE: (703)684-1111
TTELEPHONE: (703)684-1111
TTELEPHONE: (703)684-1111
TTELEPHONE: (703)684-1111
TTELEPHONE: CHARACTERIFICS:
SEQUENCE CHARACTERIFICS:
           US/07/718,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: peptide
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             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINO ACIDS
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STRANDEDNESS: sir
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       LENGTH:
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TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME FILE REFERENCE: A34762 021645.0105
CURRENT APPLICATION NUMBER: US/08/753,750B
CURRENT PILING DATE: 1996-11-29
PRIOR APPLICATION NUMBER: CA 2,164,274
PRIOR FILING DATE: 1995-12-01
PRIOR FILING DATE: 1995-12-01
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;
HASEGAMA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO
TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR
NUMBER OF SEQUENCES: 31
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/392,841
FILING DATE: 11-AUG-1989
                                                                                                                                                                                                                                                                                                                                                            63.2%; Score 24; DB 4; Length 5; 100.0%; Pred. No. 3.8e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.2%; Score 24; DB 6; Length 5; 100.0%; Pred. No. 3.8e+05; tive 0; Mismatches 0; Indels
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ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WESULT 4
US-07-718-577-6
Sequence 6, Application US/07718577
Patent No. 5432018
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Cwirla, Steven E.
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
ITLE OF INVENTION: SCREENING SYSTEMS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Street
STREET: Tower
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserva
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;Patent No. 5185431
                                                                                                                                                                                                                                                                                                                 US-08-753-750B-38
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Townsend and Townsend and Crew
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CURRENT FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 7
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                        ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 42.9
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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Best Local Similarity
Matches 3; Conserv
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   ADDRESSEE:
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                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
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                                                                                                                                                                                                                       RESULT 6
US-08-443-640-16
is Sequence 16, Application US/08443640
is Patent No. 5691140
is GENERAL INFORMATION:
APPLICANT: NOREN, CHRISTOPHER J.
ITILE OF INVENTION: BIDIRECTIONAL IN VITRO TRANSCRIPTION
ITILE OF INVENTION: DIRECTIONS
ITILE OF INVENTION: DIRECTIONS
ITILE OF INVENTION: DIRECTIONS
INVERSE NEW ENGLES 36
CORRESPONDENCE 36
CORRESPONDENCE NEW ENGLAND BIOLABS, INC
STREET: 32 TOZER ROAD
CITY: BEVERLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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; Sequence 30, Application US/08462720
; Sequence 30, Application US/08462720
; Parcent No. 58430101
; GENERAL INFORMATION:
    APPLICANT: Roberts, David D.
    APPLICANT: Stpes, Henry C.
    APPLICANT: Stpes, John M.
    APPLICANT: Guo, Neng-haa
    APPLICANT: Negre, Eric
    TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and
    TITLE OF INVENTION: Related Collagen-Binding Proteins
    NUMBER OF SEQUENCES: 30
    CORRESPONDENCE ADDRESS:
4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.2%; Score 24; DB 1; Length 7; Best Local Similarity 42.9%; Pred. No. 3.8e+05; Matches 3; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRX: US
ZIP: 01915
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,640
FILING DATE: 18-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REGISTRATION NUMBER: 30901
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MASSACHUSETTS
COUNTRY: US
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                                                                  1 GYWXXXW 7
                                                                                                                                1 GGWSKSW 7
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   Matches
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RESULT 8
US-09-388-788-2
Sequence 2, Application US/09388788
Factor No. 6429359
GENERAL INFORMATION:
APPLICANT: LAMPPA, CAYLE
TITLE OF INVENTION: PRODUCTION OF CELLULASE IN PLASTIDS OF TRANSGENIC
TITLE OF INVENTION: PLANTS
FILE REPERENCE: 21459/90301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
OTHER INFORMATION: Construct
US-09-388-788-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION UNMER:
CLASSIFICATION:
FILING DATE:
CLASSIFICATION:
NAME:
NAME:
NAME:
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: REALDE FURDED GISK
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CLASSIFICATION NUMBER: US/08/440
PTLING DATE: 28-APR-1994
ATYONEY/AGENT INFORMATION:
NAME: COCULZZI, LAULE A
REGISTRATION NUMBER: 30742
REFRENCE/DOCKET NUMBER: 7683-054
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (212) 790-9090
TELEFRAK: (212) 789-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ullich, Axel
APPLICANT: Ullich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASES PTP-D1
NUMBER OF SEQUENCES: 41
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 2; Le:
Pred. No. 3.8e+05;
1; Mismatches 1;
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 3.6
Matches 3; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Pennie & Edmonds
1155 Avenue of the Americas
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 53
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-446-345-12; Sequence 12, Application US/08446345; Patent No. 5831009; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.9%;
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Best Local Similarity 66.7
Matches 4; Conservative
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ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                               ORGANISM: Mus musculus US-09-563-222C-53
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STRANDEDNESS: sir
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STATE: N.Y.
COUNTRY: U.S.A.
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                                                                                                                            TYPE: PRT
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Sequence 53, Application US/0956322C

General Information:
General Information:
APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
CURRENT PREFERENCE: 06804-0501
CURRENT PILING DATE: 2000-05-02
CURRENT PILING DATE: 2000-05-02
PRIOR PILING DATE: 2001-05-02
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                                                                    APPLICANI: C. Brian K
KAY, Brian K
FRELINGER, Jeffrey A
HYDE-DERUYSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CORRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/069, 827A
FILING DATE: 30-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/09/060, 359
FILING DATE: 31-MAR-1998
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-OCT-1997
FILING DATE: 31-OCT-1997
FILING DATE: 31-OCT-1996
ATTORNEY/AGENT INPORMATION:
MANAL. CORDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFRAX: (202) 737-358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-069-827A-94
Sequence 94, Application US/09069827A
Patent No. 6517114
GENERAL INFORMATION:
APPLICANT: FOWLKES, Dana M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.2
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
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Gaps

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Pacquence 14, Application US/08884569A

Requence 14, Application US/08884569A

GENERAL INFORMATION:
APPLICAMT: CHIANG, MING-KO
APPLICAMT: FLANAGAN, JOHN G.
TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO FILE REFERENCE: HWV-020.01
CURRENT APPLICATION NUMBER: US/08/884,569A
CURRENT FILING DATE: 1997-06-27
PRIOR APPLICATION NUMBER: 60/021,040
PRIOR FILING DATE: 1996-07-02
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
NAME/KEY: NOD RES
LOCATION: (3) DECOMMENTION: Arg or Gln
NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                            Description of Artificial Sequence: Synthetic peptide
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66.7%; Pred. No. 3.8e+05;
tive 1; Mismatches 1;
CURRENT APPLICATION NUMBER: US/08/884,569A
CURRENT FILING DATE: 1997-06-27
PRIOR APPLICATION NUMBER: 60/021,040
PRIOR FILING DATE: 1996-07-02
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
10-109-406-264-2
; Sequence 2, Application US/09430626A
; Patent No. 6482605
; GENERAL INFORMATION:
; APPLICANT: Aoki, Naohito
; APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Description
OTHER INFORMATION: peptide
NAME/KRY: MOD_RES
LOCATION: (5)
OTHER INFORMATION: Ile or Val
US-08-884-569A-11
                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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CTHER INFORMATION: Ile or Val

US-08-884-569A-14
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Best Local Similarity 50.0
Matches 3; Conservative
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Matches 4; Conservative
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Sequence 11, Application US/08884569A

Sequence 11, Application US/08884569A

Sequence 11, Application US/08884569A

APPLICANT: CHIANG, MING-KO

APPLICANT: FLANAGAN, JOHN G.

TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO

FILE REFERENCE: HWV-020.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                 Sequence 2, Application US/08951260A
Patent No. 6004791
GENERAL INFORMATION:
APPLICANT: Abcki, Nachito
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%; Score 22; DB 3; Length 6; 66.7%; Pred. No. 3.8e+05; ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 6.5" Diskette, 1.44 Mb
COMPUTER: 1BM Comparible
OPERATING SYSTEM: 1BM Comparible
OFERTING DATE: ORCODER 16, 1997
FILING DATE: ORCODER 16, 1997
APPLICATION NUMBER: 60/030,860
FILING DATE: June 17, 1997
ATTORNEY/AGENT INFORMATION:
NAME: WARDING, 1097
ATTORNEY/AGENT INFORMATION:
NAME: WARDING, 1233 489-1600
TELEFPAN: (213) 489-1600
TELEFPONE: (213) 489-1600
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TELEFPAN: (213) 489-1600
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STREET: 633 West Fifth Street
STREET: Suite 4700
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
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Best Local Similarity
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                                                                                               US-08-951-260A-2
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Gaps

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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20 AND RELATED PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 4; Length 6; Pred. No. 3.8e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FaetESD for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,626A
FILING DATE: 29-05-19-9
CLASSIFICATION *CURNOWN>
PRIOR APPLICATION NUMBER: 08/951,260
FILING DATE: 00-05-E 16, 19-7
APPLICATION NUMBER: 06/10-860
FILING DATE: 00-06-E 16, 19-7
APPLICATION NUMBER: 00/10-860
FILING DATE: 00-06-E 16, 19-7
APPLICATION NUMBER: PCT/1897/00946
FILING DATE: June 17, 19-7
ATTORNEY/AGENT INFORMATION:
NAMME: WARDING RICHARD 3.327
REGISTRATION NUMBER: 32,327
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (213) 955-0440
                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide FEATURE:
                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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Search completed: December 29, 2004, 22:08:13 Job time : 37 secs

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sequence 65, Appl Sequence 18, Appl Sequence 195, Appl Sequence 195, Appl Sequence 1579, Appl Sequence 1579, Appl Sequence 1879, Appl Sequence 1879, Appl Sequence 187, Appl Sequence 187, Appl Sequence 196, Appl Sequence 197, Appl Sequence 197, Appl Sequence 27, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 197, Appl Sequence 198, Appl Sequence 198, Appl Sequence 198, Appl Sequence 198, Appl Sequence 198, Appl Sequence 198, Appl Sequence 198, Appl Sequence 198, Appl

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US-10-243-613-84

US-10-087-993-1

US-10-314-213-687-2

US-10-314-213-665

US-10-190-082-65

US-10-190-082-65

US-10-190-082-76

US-10-190-082-76

US-10-191-195

US-10-191-195

US-10-191-196

US-10-191-196

US-10-190-082-144

US-10-190-082-144

US-10-190-082-136

US-10-190-082-136

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US-10-190-082-136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-10-436-549-496
; Sequence 496, Application US/10436549
    Query Match
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYWXXXW 7
  TYPE: PRT
ORGANISM: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                       US-10-046-922-67
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Sequence 525, App
Sequence 525, App
Sequence 525, App
Sequence 48, Appl
Sequence 45, Appl
Sequence 38, Appl
Sequence 53, Appl
Sequence 53, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 51, Appl
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                                                      December 29, 2004, 22:01:50 ; Search time 141 Seconds (without alignments) 17.859 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                     60586
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-046-922-67
US-10-436-549-496
US-10-426-549-525
US-10-712-425-525
US-10-712-425-526
US-10-418-943-48
US-09-844-773-48
US-09-563-222-53
US-09-563-222-53
US-10-475-853-6
US-10-7783-950-53
                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                            1599051 segs, 359727711 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                  Applications AA:*
                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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                  Copyright
                                                                                                      1 GYWXXXW 7
                                                                                                                                                                                                                                  Published
                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery
Match
                                                                                              Perfect score:
                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444444444
                                                                                                      Sequence:
                                                                                                                                             Searched:
                                                                                                                                                                                                                                  Database
                                                       Run on:
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0
Sequence 67. Application US/10046922

Bublication No. US20020164667A1

GENERAL INFORMATION:
APPLICANT: Alitalo, Kari

TITLE OF INVENTION: VEGET INHIBITOR MATERIALS AND METHODS
TITLE OF INVENTION: VEGET INHIBITOR MATERIALS AND METHODS
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
CURRENT FILING DATE: 2002-01-15
SOFTWARE: PATENTIN VERSION 3.0

SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (4)..(6)
COTENTION: (5).(6)
COTENTION: X at position 4-6 is any amino acid
US-10-046-922-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.2%; Score 32; DB 13; 100.0%; Pred. No. 1.5e+06; ive 0; Mismatches 0;
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Result No.

```
APPLICANT: HISH, KANN DAVID

APPLICANT: LIVINGSTON, DAVID

APPLICANT: LIVINGSTON, DAVID

TITLE OF INVENTION: PROTECOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN

TITLE OF INVENTION: MODIFICATION ANALYSIS

FILS REFERENCE: ENGE-P02-001

CURRENT APPLICATION NUMBER: 60/379,626

PRIOR FILING DATE: 2002-07-10

PRIOR PELICATION NUMBER: 60/393,137

PRIOR PELICATION NUMBER: 60/393,137

PRIOR PELICATION NUMBER: 60/393,197

PRIOR PELICATION NUMBER: 60/393,231

PRIOR PELICATION NUMBER: 60/393,233

PRIOR PELING DATE: 2002-07-01

PRIOR PELING DATE: 2002-07-01

PRIOR PELING DATE: 2002-07-01

PRIOR PELING DATE: 2002-07-01

PRIOR PELING DATE: 2002-07-01

PRIOR PELING DATE: 2002-07-01

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NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 15; I; Pred. No. 1.5e+06; 0; Mismatches 0;
                                                                           PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/39,223
PRIOR APPLICATION NUMBER: 60/30,948
PRIOR APPLICATION NUMBER: 60/430,948
PRIOR PILING DATE: 2002-10-04
PRIOR PILING DATE: 2002-12-04
PRIOR PILING DATE: 2002-12-04
PRIOR PILING DATE: 2002-12-13
PRIOR PILING DATE: 2002-12-13
PRIOR PILING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 614
SOFTWARE: PATENTIN VORTERIOR 3.2
SEQ ID NO 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 496, Application US/10712425
Publication No. US20040180380A1
GENERAL INFORMATION:
APPLICANT: LEE, FRANK D.
                                                  APPLICATION NUMBER: 60/393,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.2%;
Best Local Similarity 100.0%;
Matches 3; Conservative 0
FILING DATE: 2002-07-01
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APPLICANT: Chan, John W.
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APPLICANT: Chan, John W.
PERCONITION ENCORED J.
TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: UNIQUE SECONITION SEQUENCES AND METHODS OF USE THE REPRENCE: ENGS-PO1-01
CURRENT APPLICATION NUMBER: 06/339, 235
PRIOR FILING DATE: 2002-07-01
PRIOR PILING DATE: 2002-07-01
PRIOR PILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/333, 230
PRIOR FILING DATE: 2002-07-01
PRIOR FILING DATE: 2002-07-01
PRIOR PILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 60/433, 319
PRIOR PILING DATE: 2002-12-07-01
PRIOR FILING DATE: 2002-12-07-01
PRIOR FILING DATE: 2002-12-07-01
PRIOR FILING DATE: 2002-12-07-01
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## Squence 525, Application No. US20040038307A1
## GENERAL INPORMATION:
## APPLICANT: Lee, Frank D.
## APPLICANT: Chan, John W.
## APPLICANT: Chan, John W.
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Publication No. US20040038307A1
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                          APPLICANT: Lee, Frank D.
APPLICANT: Meng, Dr. Xun
APPLICANT: Chan, John W.
                                                  GENERAL INFORMATION:
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CRGANISM: Human
US-10-436-549-496
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RESULT 7

US-10-346-737A-45

Sequence 45, Application US/10346737A

Sequence 45, Application US/10346737A

Publication No. US20040142379A1

GENERAL INFORMATION:

APPLICANT: St. Hilaire, Phaedria

TILLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS

FILE REFERENCE: 11225.16US01

CURRENT APPLICATION NUMBER: US/10/346,737A

CURRENT FILING DATE: 2003-01-16

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.1

SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38, Application US/09884767A

Publication No. US20020192789A1

GENERAL INFORMATION:

APPLICANT: DAX Corp.

APPLICANT: Ladner, Nobert C.

APPLICANT: Ladner, Nobert C.

TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES

FILE REFERENCE: DXX-012.1 US, DYX-012.1 PCT

CURRENT APPLICATION NUMBER: US/09/884,767A

CURRENT FILING DATE: 2000-06-19

PRIOR APPLICATION NUMBER: US 09/597,321

PRIOR FILING DATE: 2000-06-19

NUMBER OF SEQ ID NOS: 217

SEQ ID NOS: 217

SEQ ID NOS: 217

SEQ ID NOS: 217

SEQ ID NOS: 217

SEQ ID NOS: 217
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; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-38
                                                                                                                                                                                                 Length 6;
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                                                                                                                                                                                          63.2%; Score 24; DB 15;
50.0%; Pred. No. 1.5e+06;
iive 0; Mismatches 3;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Peptide
US-10-346-737A-45
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Matches 3; Conservative
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; SEQ ID NO 48
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo Bapiens
US-10-418-943-48
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                                                                                                                                                                                                                                         Sequence 525, Application US/10712425
Sequence 525, Application US/10712425
Sequence 525, Application No. US20040180380A1
GENERAL INFORMATION:
APPLICANT: LEE FRANK D
APPLICANT: LIVINGSTON DAVID
APPLICANT: LIVINGSTON DAVID
TITLE OF INVENTION: MODIFICATION NALYSIS
FILE REFERENCE: EMES-D02-01
TITLE OF INVENTION: MODIFICATION NAMER: US/10/712,425
CURRENT PELING DATE: 2003-011-13
FRIOR PELICATION WHMER: (6/39),137
FRIOR FILING DATE: 2002-07-01
FRIOR FILING DATE: 2002-07-01
FRIOR FILING DATE: 2002-07-01
FRIOR FILING DATE: 2002-07-01
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FRIOR APPLICATION WHMER: (6/393,23)
FRIOR FILING DATE: 2002-07-01
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US-10-418-943-48
; Sequence 48, Application US/10418943
; Publication No. US20040002441A1
; GENERAL INFORMATION:
; APPLICANT: Segall, Anca
; APPLICANT: Pinilla, Clemencia
; TITLE OF INVENTION: RECOMBINATION MODULATORS AND METHODS
; TITLE OF INVENTION: FOR PRODUCING AND USING THE SAME
; FILE REFERENCE: 011443 008-99
; CURRENT APPLICATION NUMBER: US/10/418,943
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 09/602,087
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 3; Conservative
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Publication 0. VB20040259829A1
Publication NO. VB20040259829A1
Publication NO. VB2004025982A1
Publication NO. VB2004025982A1
Publication NO. VB2004025982A1
APPLICANT: Danks, Mary K.
APPLICANT: Potter, Philip M.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of TITLE OF INVENTION: Tumor Cells
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of TITLE OF INVENTION: UNMBER: US/10/858,271
CURRENT APPLICATION NUMBER: US/09/595,682
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/075,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 53, Application US/10783950

publication No. US20040199945A1

GENERAL INFORMATION:
APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
TITLE OF INVENTION: IMMUNGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 066904-0501
CURRENT PELIGN DATE: 2004-02-19
CURRENT PELIGN DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
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63.2%; Score 24; DB 16; I
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: peptide derived from chit36
US-10-475-853-6
                                CURRENT APPLICATION NUMBER: US/10/475,853
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 20
SOFWRAKE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Mus musculus
US-10-783-950-53
FILE REFERENCE: 27049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GYW 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GYW 3
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                                                                                                                                                                                                                                                     TYPE: PRT
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Publication No. US20040121442A1
GENERAL INFORMATION:
APPLICANT: Chet, Ilan
APPLICANT: Viterbo, Ada
TITLE OF INVENTION: RECOMBINANT FUNCAL CHITINASES, POLYNUCLECTIDE SEQUENCES ENCODING
TITLE OF INVENTION: PROMOTERS OF SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/10403938

Sequence 27, Application US/10403938

Publication No. US20040025195A1

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
TITLE OF INVENTION: BGS.19

FILE REFERENCE: D0227 NP

CURRENT FILING DATE: 2003-03-28

PRIOR APPLICATION NUMBER: U.S. 60/368,422

PRIOR FILING DATE: 2002-03-28

PRIOR FILING DATE: 2002-03-28
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hatt, Andrew
APPLICANT: Hatt, Andrew
APPLICANT: Hein, Mich B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: EUKARYOTIC CELLS
FILE REPERENCE: 310098.406
CURRENT APPLICATION NUMBER: US/09/563,222
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.2%; Score 24; DB 10; Length 7; 100.0%; Pred. No. 1.5e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                             US-09-563-222-53
Sequence 53, Application US/09563222
Publication No. US20030079253A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 27
LENGTH: 7
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Best Local Similarity 100.
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ORGANISM: Homo sapiens
US-10-403-938-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222-53
                                              GYW 3
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                                                                                                                          ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION WUMBER: 32,327
REPERENCE/DOCKET NUMBER: 225/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: December 29, 2004, 22:13:17 Job time : 142 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for an unspecified amino acid. SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 17; Length 7;
Pred. No. 1.5e+06;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 84, Application US/10243613;
Publication No. US20040053823A1;
GENERAL INFORMATION:
APPLICANT: Smith, Jeffrey W.
APPLICANT: Smith, Jeffrey W.
APPLICANT: Kridel, Steven J.
TITLE OF INVENTION: Selective Substrates for Matrix, TITLE OF INVENTION: Metalloproteinases
FILE REFERENCE: P-LJ 5432
CURRENT APPLICATION NUMBER: US/10/243,613
CURRENT APPLICATION NUMBER: US 09/953,592
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aoki, Naohito
Kim, Yeong Woong
Wang, Hong Yang
Chen, Zhengjun
Naylor, Oliver
Kharitonenkov, Alexei Igorevich
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PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: PCT/US99/03171
PRIOR FILING DATE: 1999-02-12
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STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: synthetic construct
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US-10-087-993-1
; Sequence 1, Application US/10087993
; Publication No. US20020169303A1
; GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Ullrich, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL PTP20
                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-858-271-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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Best Local Similarity 33.3%;
Matches 2; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                            NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 7
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---a 2; Conservative
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dermorphin - Rohde
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bradykinin-potenti
RPCH-related neuro
T-cell receptor be
T-cell receptor be
cholecystokinin-5
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Ig heavy chain CRD
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T-cell receptor be
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                                                                    December 29, 2004, 21:57:34 ; Search time 38 Seconds (without alignments) 17.724 Million cell updates/sec
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version 5.1.6
- 2004 Compugen Ltd.
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                                                                                                                                                                                                          283416 segs, 96216763 residues
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Maximum Match 100%
Listing first 45 summaries
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S21230
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A60803
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PT0519
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Gapop 10.0 , Gapext 0.5
  GenCore (c) 1993 .
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2: pir2:*
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4: pir4:*
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seq length: 7
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Perfect score:
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Maximum DB &
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PT0637 PT0641 PT0641 PT0726 PT0968 PT0028 PT0028 PT0528 PT0628 PT0628 PT0628 PT0628 PT0628 PT0628	ALIGNMENTS ese eel mica (Japanese eel) ruence_revision 31-Mar-1992 #t Kubota, I.; Muneoka, Y.; And formun. 180, 828-832, 1991 unction of a partapoptide iso 53; MUD:92062113; PMID:19537 increased basal tone of the c increased basal tone of the c iscle of the gastro-intestinal	Score 20; DB Pred. No. 2.8 1; Mismatches	on (10 n 17-i 1 T ce 7601;	Score 15; DB Pred. No. 2.8 0; Mismatches
0000004000000000	eel (Jap (Gap (e_rev (ota, no.1) (ion o MUID:	4.4	D-J e me - rev 91 of UID: wn	7 86 ;
000000000000000000000000000000000000000	eptide - Japanese eel Anguilla japonica (JapaneseMar-1992 #sequence_revision T.; Ikeda, T.; Kubota, I.; M. Niophys. Res Commun. 180, 822 Etructure and function of a per enumber: JH0253; MUID: 920621 nr: JH0253 stype: protein s: 1-5 <ues> nra</ues>	52.6%; larity 66.7%; Conservative 3	t chain V-D-J llus (house m #sequence_re S-124, 1991 sequences of pro509; MUID pn not shown pn pn pn pn pn pn pn p	39.5%; larity 66.7%; Conservative
0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.	- Jap 992 #5 253 #5 253 eda, T eda, T re and er: JH 253 prote vuts.	h Similarity 2, Conserv 1 GYW 3 	ttor beta chain us musculus (ho ul-1992 #sequen Pr0532 174, 115-124, ctional sequenc number: Pr059; Pr0532 ansalation not sype: mRNA 1-6 <fee adul="" al="" r-cell="" receptor<="" source:="" td=""><td>Similarity 2; Conser</td></fee>	Similarity 2; Conser
=======================================	T.T. 1 pentapeptide - Japanese eel pecies: Anguilla japonica (Jule: 31-Mar-1992 #sequence_r cession: JH0253 #sequence_r in them. Biophys. Res. Commun. the: Structure and function iference number: JH0253; MUI cessation: JH0253; MUI septides: 15 <ues></ues>	fatch cal Simil 3 2; C 1 GYW 1 GFW	RESULT 2 PT0532 T-cell receptor beta chain V-D-J regi C; Species: Mas musculus (house mouse) C; Accession: PT0532 R; Peeney, A.J. J. Exp. Med. 174, 115-124, 1991 A; Title: Junctional sequences of feta A; Reference number: PT0599; MUID:9127 A; Accession: PT0532 A; Status: translation not shown A; Molecule type: mRNA A; Residues: 1-6 < FEE> A; Experimental source: adult thymus, C; Reywords: T-cell receptor	atch cal
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	RESULT 1 JH0253 gut pentapeptide - Japanee C,Species: Anguilla japoni C,Odte: 31-Mar-1992 #seque C,Accession: JH0253 R,Uesaka, T.; Ikeda, T.; F Blochen: Blophys. Res. Con A,Title: Structure and fur A,Reference number: JH0253 A,Accession: JH0253 A,Accession: JH0253 A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues 1-5="" <ues="" a,residues:=""> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues> A,Residues: 1-5 <ues 1-5="" <ues="" <ues<="" a,residues:="" td=""><td>Query Match Best Local 8 Matches 3 Qy 1</td><td>RESULT 2 T-0611 receptor C.Species: Mus C.Accession: PT-01. V. Exp. Med. 17 A.Title: Juncti A.Title: Juncti A.A.Reference nu A.A.Reference nu A.A.Reference nu A.A.Reference nu C.A.Reference nu C.A.Reference nu C.A.Reference nu C.A.Reference nu C.A.Reference nu C.A.Residues: 1-6 A.Experimental C.Keywords: T-C.</td><td>Query Match Best Local : Matches</td></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues></ues>	Query Match Best Local 8 Matches 3 Qy 1	RESULT 2 T-0611 receptor C.Species: Mus C.Accession: PT-01. V. Exp. Med. 17 A.Title: Juncti A.Title: Juncti A.A.Reference nu A.A.Reference nu A.A.Reference nu A.A.Reference nu C.A.Reference nu C.A.Reference nu C.A.Reference nu C.A.Reference nu C.A.Reference nu C.A.Residues: 1-6 A.Experimental C.Keywords: T-C.	Query Match Best Local : Matches

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tubulin beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S33567
B;Hinz, U.; Wolk, A.; Renkawitz-Pohl, R.
Development 116, 543-554, 1992
A;Fitle: Ultrabithorax is a regulator of beta-3 tubulin expression in the Drosophila visc A;Reference number: S33567; WUID:93170162; PMID:1363225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P08841; EMBL:X68393; NID:g7669; PIDN:CAA48459.1; PID:g4377448
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N;Alternate names: 11S globulin alpha subunit gamma chain
N;Alternate names: 11S globulin alpha subunit gamma chain
C;Species: Cucurbita sp. (cucurbit)
C;Accession: 809478
R;Ohmiya, M; Hara, I: Matsubara, H.
R;Ohmiya, M; Hara, I: Matsubara, H.
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and A;Reference number: 809066
                                                                                                                                                                                                                                                                                                                                                                                 J. Exp. Med. 174, 115-124, 1991
A;Title: Unactional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0728
A;Steuts: translation not shown
A;Molecule type: DNA
A;Residues: 1-7 <FEE>
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0728
R;Feeney, A.J.
  Gaps
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Similarity 50.0%; Pred. No. 2.8e+05;
1; Conservative 1; Mismatches 0;
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C;Keywords: T-cell receptor
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Pred. No. 2.8e+05;
0; Mismatches 1;
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  Mismatches
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A;Cross-references: FlyBase:FBgn0003888
A;Introns: 5/3
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Best Local Similarity 66.7%;
Matches 2; Conservative
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                                                                            C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C;Chan; W.Y.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.E Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal max A;Reference number: A35640; MUID:90222173; PMID:2326268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
c;Species Phyllomedusa bicolor (two-colored leaf frog)
C;Species Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C;Accession: S21230
C;Accession: G:; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G. FEBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of the A;Reference number: S21152; MUID:92339502; PMID:1633846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0629
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A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
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A;Molecule type: mRNA
A;Rosidues: 1-6 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH
A;Accession: PT0528
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A;Molecule type: mRNA
A;Residues: 1-6 <FE2>
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB
C;Keywords: T-cell receptor
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0; Mismatches 1; Indels
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                                                        cerebellar degeneration-related protein - mouse (fragment)
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-6 < CHE>
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C;Accession: A60139
R;Hardia, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
Biochim. Biophys. Acta 828, 380-382, 1985
Biochim. Biophys. Acta 828, 380-382, 1985
A;Title: Amino acid sequence around the reactive serine residue of the thioesterase doma; A;Title: Amino acid sequence around the reactive serine residue of the thioesterase doma; A;Accession: A60139; MUD:85175165; PMID:3921056
A;Accession: A60139
A;Molecule type: protein
A;Residues: 1-7 cHAR>
C;Superfamily: rat fatty-acid synthase; 3-oxoacyl-(acyl-carrier-protein] synthase I homolydy: short-crain alcohol dehydrogenase homology; [acyl-carrier-protein] S-n C;Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enzy F;5/Active site: Ser (of oleoyl-(acyl-carrier-protein] hydrolase) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sylathione transferase (EC 2.5.1.18) class mu 9 - pig (fragment)

NyAlternate names: glutathione S-transferase class mu 9
Cispecies: Sus acrofa domestica (domestic pig)
Cispecies: Sus acrofa domestica (domestic pig)
Cispecies: Sus acrofa domestica (domestic pig)
Cispecies: Sus acrofa domestica (domestic pig)
Cispecies: Sus acrofa domestica (domestic pig)
Cispecies: Sus acrofa domestica (domestic pig)
RyRoulmi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J. 317, 879-884, 1996
A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray
A;Reference number: S71864; MUID:96332484; PMID:8760377
A;Recession: S71870
A;Residues: 1-7 <ROUS
C;Comment: At least five species-independent classes of cytosolic glutathion transferases
C;Comment: At least five species-independent classes of cytosolic glutathion transferases
C;Complex: dimer
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C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Species: S3662
R;Mignogna, G:; Severini, C:; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.;
FEBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of the
A;Reference number: S21152; MuID:92339502; PMID:1633846
A;Reference prediminary
A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
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Int. J. Pept. Protein Res. 17, 316-321, 1981
A;Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz A;Reference number: A61324; MUID:82029915; PMID:7287302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattue norvegicus (Norway rat)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C;Datesesion: A64411
R;Burzynski, S.R.
Anal. Biochem. 70, 359-365, 1976
A;Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the A;Reference number: A61411; MUID:76182447; PMID:1267130
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fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
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Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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100.0%; Pred. No. 2.8e+05;
iive 0; Mismatches 0;
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iive 0; Mismatches 0;
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
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A;Residues: 1-6 <BUR>
C;Superfamily: unassigned animal peptides
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Best Local Similarity 100.
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A,Accession: S09478
A,Molecule type: protein
A,Residues: 1-4 <OHM>
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A; Status: preliminary
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RESULT 15
A34626
RPCH-related neuropeptide - ferruginous spindle
C;Species: Fusinus ferrugineus (ferruginous spindle)
C;Species: Fusinus ferrugineus (ferruginous spindle)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C;Accession: A34626
R;Kuroki, Y; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A;Reference number: A34626
A;Reference number: A34626; MuID:90179762; PMID:2310394
A;Accession: A34626
A;Residues: preliminary
A;Molecule type: protein
A;Residues: 1-4 <KUR>
C;Reywords: neuropeptide
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P37196
P37196
Bardykinin-potentiating peptide 6 - island jararaca
C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: P37196
A;Cintra, A-C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides 1, A;Reference number: A37196, MUID:90351557; PMID:2386615
A;Accession: F37196
A;Accession: F37196
A;Accession: F37196
A;Accession: Gardy A;Accession: Gardy A;Residues: 1-3 <CINS
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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34.2%; Score 13; DB 2; Length 7; 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 1; Conservative
Query Match 34.2
Best Local Similarity 100.
Matches 2; Conservative
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SEQUENCE FROM N.A.

TISSUB=Ovary;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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(c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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allium asca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
TISSUB=Fibroblast;
MEDLINE=95009907; PubMed=7523108;
METALINE=95009907; Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Merrick B.A., Patterson R.M., Wichter L.L., and novel murine proteins using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.6, its MW is: 19 kDa.
Direct protein sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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01-OCT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Unknown protein from 2D-PAGE of fibroblasts (PI9) (Fragment).
Mus musculus (Mouse).
                 P01373
P8261
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Last annotation update)
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               PRCT_PERAM
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ASP_LACSN
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ALLG_CARNA
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E105_LITRU
FAR2_ASCSU
FAR3_HAECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Cree Ol-JUN-2001 (TrEMBLrel. 17, Last Ol-MAR-2004 (TrEMBLrel. 26, Last SQSTM1 protein. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Ci Mammalia; Eutheria; Primates; Cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 40.0 hes 2; Conservative
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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WIGRW 5
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Craniata, Vertebrata, Euteleostomi, Catarrhini, Hominidae, Homo.

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1; Conservative
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                                                                                                                                                                                                                                                                                                  STANDARD;
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Best Local Similarity
                     than Ocp-3.
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P30425;
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                                                                                                                                                                                                                                                                                                GWA SEPOF
P83570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE,
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GWA_SEPOF
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      $25555$E$
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                                                                                                                                                                                                                                                                                            Strausberg R;
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005887; AA405857.3;
GO; GO:0005829; C:cytosol; ISS.
GO; GO:0042169; F:SH2 domain binding; ISS.
GO; GO:004130; F:SH2 domain binding; ISS.
GO; GO:004130; F:SH2 domain binding; ISS.
GO; GO:004130; F:Cubiquitin binding; ISS.
GO; GO:004242; P:Intracellular signaling cascade; ISS.
GO; GO:0045944; P:Postellular signaling cascade; ISS.
GO; GO:0008104; P:Posteln localization; ISS.
GO; GO:0008104; P:Protein localization; ISS.
GO; GO:0008104; P:Protein localization; ISS.
GO; GO:0008104; P:Protein localization; ISS.
GO; GO:0008104; P:Protein localization; ISS.
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Perange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bolffard G.G., Blakesley R.W., Oruchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                            Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
MEDLINE=20336815; PubMed=10876044;
IwakbLINE=20336815; PubMed=10876044;
Iwakoati E., Hisada M., Minakata H.;
Iwakoative peptides isolated from the brain of a Japanese octopus, Octopus minor.";
Peptides 21:623-630(2000).
-i- FUNCTION: Cardioactive; has both positive chronotropic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Cardioactive peptides Ocp-3/Ocp-4.
Cotopus minor (Octopus).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 42.1%; Score 16; DB 2; Length 7; Local Similarity 66.7%; Pred. No. 1.8e+06; nes 2; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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737728769DDDD6F0 CRC64;
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InterPro; IRR000433; Znf_ZZ.
Pfam; PR00569; ZZ. 1.
SMART; SM00165; UBA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50030; UBA; 1.
PROSITE; PS01357; ZF ZZ 1;
PROSITE; PS50135; ZF ZZ 2;
SEQUENCE 7 AA; 779 MW;
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ID OCP3 (
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR DOCATION: Secreted.
-!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI; RANGE=1-4; NOTE=Ref.1.
-- MD-mino acid, Direct protein sequencing; Hormone.
MOD_RES 2 2 D-serine (in form Ocp-4).
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notropic effects on the heart. Ocp-4 is a 1000 time less active
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01-FEB-1994 (Rel. 28, Last sequence update)
05-VUL-2004 (Rel. 44, Last annotation update)
Bradykinin-potentiating peptide S5,2 (SA) (Angiotensin-converting enzyme inhibitor).
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                                                                                                                                                                                                    Query Match 39.5%; Score 15; DB 1; Length 4; Best Local Similarity 66.7%; Pred. No. 1.8e+06; Matches 2; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION, MASS SPECTROMETRY, AND AMIDATION
                                                                                                                                                           SEQUENCE 4 AA; 463 MW; 6AB365B81000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Sepia officinalis (Common cuttlefish).
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NCBI_TaxID=6610;
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PIR; A58512; A58512.
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Best Local Similarity
Matches 1; Conserv
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                    NCBI_TaxID=7004;
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ID BRHP CONIM
AC P58803;
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Matches
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TISSUE=Venom;

WEDLINE=90351557; PubMed=2386615;

Cintra A.C.O., Vieira C.A., Giglio J.R.;

Cintra A.C.O., Vieira C.A., Giglio J.R.;

Cintra A.C.O., Vieira C.A., Giglio J.R.;

Thimary structure and biological activity of bradykinin potentiating to peptides from Bothrops insularis snake venom.";

J. Drotein Chem. 9:221-227(1990).

J. Protein Chem. 9:221-227(1990).

J. Protein Converting enzyme and enhances the action of anglotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.

PIR: G37196; G37196.

RW Pyrrolidone carboxylic acid.

Drivel Pire Carboxylic acid.

Purrolidone carboxylic acid.
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Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella.";
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-!- TISSUE SPECIFICITY: Skin.
Amidation; Amphibian defense peptide; Direct protein sequencing
MOD RES 6 6 Methionine amide.
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Locusta migratora, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Orthoptera, Caelifera, Acridomorpha,
Acridoidea, Acrididae, Oedipodinae, Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD RES 1 1 Pyrrolidone carboxylic acid. SEQÜENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.9%; Score 11; DB 1; Length 5; 100.0%; Pred. No. 1.8e+06; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.9%; Score 11; DB 1; Length 6; 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                           "Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, primary structure and synthesis.";
Regul. Pept. 37:49-57(1992).
-!- FUNCTION: Myotropic peptide. May be important in the stimulation of ion transport and inhibition of diuretic activity in Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A novel post-translational modification involving bromination of tryptophan. Identification of the residue, L-6-bromotryptophan, in peptides from Conus imperialis and Conus radiatus venom.", J. Biol. Chem. 272:4669-4688 (1997).

-!- FUNCTION: Does not elicit gross behavioral symptoms when injected centrally or peripherally in mice.

-!- SUBCELMULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Expressed by the venom duct.

-!- MASS SPECIFICITY: Expressed by the venom duct.
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Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
      MEDLINE=92262851; PubMed=1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.9%; Score 11; DB 1; Length 6; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                               PIR; A61068; A61068.
Amidation; Direct protein sequencing; Neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                           MOD RES 6 6 Glycine amide.
SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amidation; Bromination; Direct protein sequencing;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-monheptapeptide Im.
Conus imperialis (Imperial cone).
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TISSUE=Corpora cardiaca;
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P35919;
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-!- MASS SPECIFORMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
Amidation; Amphibian defense peptide; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
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-!- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen T.B., Orr D.F., Shaw C.; "Pachymedusa dacnicolor tryptophyllin-1 (PdT-1): structural characterization, pharmacological activity and cloning of precursor
                                                                                                                                                                                                                                                   Pachymedusa dacnicolor (Giant mexican leaf frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Phyllomedusinae; Pachymedusa.
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Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
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794 MW; 7772D37DC7776350 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
29-ULJ-2004 (Rel. 44, Last annotation update)
Tryptophyllin-1 (PdT-1).
                                                                                                     7 AA.
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Litoria rubella (Desert tree frog)
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Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI TaxID=6530;
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Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
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TISSUB-Ganglion;
MEDLINE=93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
Minakata H., Ikeda T., muneoka Y., Kobayashi M., Nomoto K.;
Minakata H., Ikeda T., muneoka Y., Kobayashi M., Nomoto K.;
Minakata H., 2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.",
FEBS Lett. 323:104-108(1993).
FEBS Lett. 323:46;
Amidation; Direct protein sequencing; Neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.; "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica."; PEBS Lett. 323:104-108(1993).
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Neuropeptide, Pyrrolidone carboxylic acid.
MOD_RES 1 Pyrrolidone carboxylic acid.
MOD_RES 7 AA-983 MW; 7401E9D3676046B0 CRC64;
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                                                                                                                                     Length 7;
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MOD RES 7 7 Tryptophan amide.

SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;
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                                                                                                                                     DB 1; Le
1.8e+06;
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01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
WWamide-1.
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100.0%; Pred. No. ...
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Query Match 28.9
Best Local Similarity 100.
Matches 1, Conservative
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Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
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MEDLINE=93265912; PubMed=8495720;
Minakata H., Ikeda T., Munecka Y., Kobayashi M., Nomoto K.;
"WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African glant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
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MEDLINE=81069885; PubMed=6254986;
Bonitz S.G., Coruzzi G., Theleld B., Tzagoloff A., Macino G.;
Bonitz S.G., Coruzzi G., Theleld B., Tzagoloff A., Macino G.;
"Assembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytobrome oxidase.";
J. Biol. Chem. 255:11927-11941(1980).
EMBL; V00694; CAAA24066.1; -..
GO: GO:0005739; C:mitochondrion; IBA.
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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                                                 Query Match 28.9%; Score 11; DB 1; Length 7; Best Local Similarity 100.0%; Pred. No. 1.8e+06; Matches 1; Conservative 0; Mismatches 0; Indels
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MOD_RES
Tryptophan amide.
SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Inside intron 5 (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
  7 AA; 964 MW; 7362D5B686D32310 CRC64;
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7 AA; 859 MW; 75B7232362CDC460 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 19, Last sequence update)
01-JUN-1998 (TrEMBLrel. 19, Last annotation update)
01-JUN-2010 (TrEMBLrel. 19, Last annotation update)
01-JUN-2010 (TrEMBLrel. 19, Last annotation update)
Glycine max (Soybean).
Glycine max (Soybean).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosids,
eurosids 1; Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine.
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MEDLINE=91367679; PubMed=1891369;
Laux T., Goldberg R.B.;
"A plant DNA binding protein shares highly conserved sequence motifs with HMG-box proteins.";
Nucleic Acids Res. 19:4769-4769(1991).
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28.9%; Score 11; DB 2; Length 7; 100.0%; Pred. No. 1.8e+06; Live 0; Mismatches 0; Indels
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Mahalingam R., Knap H.T.;
Submitted (FEB-1998 to the EMBL/GenBank/DDBJ databases.
EMBL; AF047050, AAC03556.1; -.
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SEQÜENCE 7 AA, 850 MW; 6AAAAAB378637810 CRC64;
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Best Local Similarity 100.04
Matches 1; Conservative
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version 5.1.6
- 2004 Compugen Ltd.
GenCore (c) 1993
           Copyright
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OM protein - protein search, using sw model

December 30, 2004, 12:55:07; Search time 48.7358 Seconds (without alignments) 51.525 Million cell updates/sec Run on:

US-10-046-922-67 38 Title: Perfect score:

1 GYWXXXW 7 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*geneseqp1990s:*geneseqp2000s:*geneseqp2001s:* A_Geneseq_23Sep04:* **Database**:

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* ........

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Aab99759 Rhesus D	Aab99769 Rhesus D	Aau03644 Group B S	Abu21589 Protein e	Abu38334 Protein e	Abu24881 Protein e	Abp30560 Streptoco		Abu29756 Protein e	Adc97241 E. faeciu	Abp26968 Streptoco		Abb55385 Lactococc	Abo74582 Pseudomon	Abu22414 Protein e	Ada49403 Multi-epi	Ado24081 Epigene c	Abo70593 Pseudomon	Abp53931 VEGFR-3 b	Abp53932 VEGFR-3 b	Aao13595 Human pol	Aar15437 Heavy cha	Abo27261 ICAM-1 bi	Abo27269 ICAM-1 bi	Abo27263 ICAM-1 bi
COLUMNIA	ID	AAB99759	AAB99769	AAU03644	ABU21589	ABU38334	ABU24881	ABP30560	ABU40245	ABU29756	ADC97241	ABP26968	ABB55389	ABB55385	ABO74582	ABU22414	ADA49403	ADO24081	AB070593	ABP53931	ABP53932	AA013595	AAR15437	AB027261	AB027269	AB027263
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фP	Query	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	86.8	86.8	86.8	86.8	86.8	86.8	86.8
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### ALIGNMENTS

Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; idiopathic thrombocytopaenic purpura; immunoglobulin. Rhesus D antibody binding peptide SEQ ID NO:4. AAB99759 standard; peptide; 10 AA. (first entry) 21-SEP-2001 AAB99759; 

Homo sapiens.

99EP-00122858. 17-NOV-1999; 13-JUN-2001.

EP1106625-A1.

99EP-00122858 (ZLBB-) ZLB BIOPLASMA AG. 17-NOV-1999;

Miescher S,

Hofmann A, Fisch I;

WPI; 2001-383568/41.

Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease newborn (HDN)

of the

Claim 1; Page 12; 19pp; English.

The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (MI) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are mimotopes which differ in their amino acid sequence from the amino acid

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perquences of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (I) is used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. haemolytic disease of the newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes peptides capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (MI) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease of the
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; herapy; prophylaxis; heamolytic disease of the newborn; HDN; ITP; cyclic; idiopathic thrombocytopaenic purpura; immunoglobulin; circular.
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                                                                                                                                                                                                                                 4; Length 10;
                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                 Score 34; DB 4
Pred. No. 9.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhesus D antibody related peptide #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 1.12
                                                                                                                                                                                                                                                                                                                                                                                                                            AAB99769 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 8; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fisch
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                                                                                                                                                                                                                                 89.5%;
57.1%;
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Best Local Similarity 57.1%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-383568/41.
                                                                                                                                                                                                                                                                                                    GYWXXXW
                                                                                                                                                                                                                                                                                                                                         GYWSAKW
                                                                                                                                                                                              Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 newborn (HDN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB99769;
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mimotopes which differ in their amino acid sequence from the amino acid sequences of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (I) is used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. haemolytic disease of the newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B. The present sequence represents an anti-Rhesus D (RhD) antibody related peptide which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus an encapsulated bacterium which is a major pathogen of humans causing sepsis and meningitis in neonates as well as adults. The S. agalactiae antigenic polypeptides are used to vaccinate against Group B Streptococcus infections, particularly to prevent infection in new born children arising from the maternal genital tract. An immunogenic composition is useful in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection. The invention does not have the disadvantages of varied response rate associated with prior art capsid polysaccharide vaccination against Group B Streptococcus
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus infections, particularly to prevent infection in neonatals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group B Streptococcus, encapsulated bacterium; therapeutic; sepsis; meningitis; neonate; antigenic; vaccine; infection; genital tract; capsid polysaccharide vaccination.
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                                                                                                                                                                                                                                                                                                                          4; Length 12;
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                                                                                                                                                                                                                                                                                                                        Score 34; DB 4
Pred. No. 12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU03644 standard; protein; 452 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2000; 2000WO-GB003437.
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ilarity 57.1%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-316444/33.
N-PSDB; AAS07061.
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                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     1 GYWXXXW
                                                                                                                                                                                                                                                                                                                                                                                                                                              GYWSAKW
                                                                                                                                                                                                                                                                                      Sequence 12 AA;
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Matches
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(1) a vector comprising a promoter operably linked to the mucleic acid conciding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a compound that influences the activity of the gene in an operon required for proliferation, (7) identifying a compound that inhibits cellular proliferation (8) identifying a gene required for that has an activity against a biological pathway in which a proliferation required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene or verexpressed or underexpressed; (12) determining the extent to the which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
                                                                                                               Gaps
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                                                                                                             ;
                                                                Score 34; DB 4; Length 452;
Pred. No. 3.6e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #7116.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 49513; 1766pp; English
                                                                                                                                                                                                                                                                                                                     ABU21589 standard; protein; 466 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-034223P.
08-FEB-2002; 2002US-00072851.
                                                                  89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-2003 (first entry)
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                                                                                                             4; Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-029926/02
N-PSDB; ACA25459.
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                                                                  Query Match
Best Local Similarity
                                                                                                                                                        1 GYWXXXW 7
                                                                                                                                                                                                  92 GYWLSAW
                     Sequence 452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200277183-A2
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                         identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an open required for
proliferation of an organism. The antisense nucleic acids are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.5%; Score 34; DB 6; Length 466; 57.1%; Pred. No. 3.8e+02; ive 0; Mismatches 3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #23861.
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU38334 standard; protein; 472 AA.
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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06-MAR-2002; 2002US-0362699P.
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Matches 4; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 466 AA;
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Wall D,
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ABU38334
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drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
the gene product or that has an activity against a biological pathway itequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound, a activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of a trains or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                             89.5%; Score 34; DB 6; Length 472; 57.1%; Pred. No. 3.8e+02;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #10408.
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU24881 standard; protein; 474 AA.
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342939P.
08-PEB-2002; 2002US-00072851.
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Trawick JD,
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N-PSDB; ACA28751.
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Wall D,
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ABU24881
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC choopitaling a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid cencoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated of polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway to the proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation and antibiot; (10) profiling a compound; activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound; activity, (11) a culture comprising strains in which the gene comprises or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids for cellular proliferation to isolate candidate molecules for rational compound and not form part of the present sequence is encoded by one of the target prowary of the present sequence is encoded by near of the present sequence again for thi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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(GENO-) INST GENOMIC RES.
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Matches 4; Conserv
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Tettelin H;

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                                                                                                                       The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5481 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a streptococcus ample. (I) is used to detect Streptococcus in a composition comprising (I) or a nucleic acid encoding (I), may be used to accompliantly produce (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to cid encoding (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                 New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                     89.5%; Score 34; DB 5; Length 475; 57.1%; Pred. No. 3.8e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by Prokaryotic essential gene #25772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck R,
Yamamoto R,
                                                                                                  Claim 1; Page 4161; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU40245 standard; protein; 475 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
9EEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-03628991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001, 2001US-00815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.1
Les 4; Conservative
                                                                                                                                                                                                                                                                                                                                      Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zamudio C,
Trawick JD,
             2002-352536/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 GYWLSAW 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ACA44115
                                                                                                                                                                                                                                                                                                                                                              Sequence 475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU40245;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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the invention traces of the production of a cell. Also included are:

the foll antisense sequences given in the specification where expression

of the nucleic acid inhibits proliferation of a cell. Also included are:

concluding a polypeptide whose expression is inhibited by the antisense acid;

concluding a polypeptide whose expression is inhibited by the antisense concluded are:

concluding a polypeptide whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular concluding the polypeptide; (6) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an accivity against a biological pathway or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway or which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound activity, (11) a culture compound that inhibits proliferation of an compound activity, (12) profiling a compound activity, (13) aculture compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for for disolar equilar proliferation of an organism. The antisense moleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for the dentifier acids are useful for dentifying proteins or screening for homologous nucleic acids required for the dentifier acids and delegant and dentifier and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and delegant and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
New antisense nucleic acids, useful for identifying proteins or screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                         for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #15283.
                                                                                                                                                    Claim 25; SEQ ID NO 68169; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU29756 standard; protein; 475 AA.
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
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Best Local Similarity 57.1.
A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 GYWISAW 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 475 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2
06-SEP-2001; 2
25-OCT-2001; 2
08-FEB-2002; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-2003
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97US-0051571P 98US-0085598P 98US-00107532

Bush D;

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New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 6868; 243pp; English
                                                                                                                                                                          (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                             2003-799836/75.
                                                                                                                                                                                                          Doucette-Stamm LA,
                                                                                                                                                                                                                                           WPI; 2003-799836
N-PSDB; ADC93587
                US6583275-B1.
                                                                                     30-JUN-1998;
                                                                                                                     02-JUL-1997;
14-MAY-1998;
                                                  24-JUN-2003
                                                                                                                                                                                                                                                                                                                                                    infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP26968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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                                                                                                                                                                                                                                                                                        the invention trained by an included and where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proniferation of a cell. Also included are:

(1) a vector comprising a proliferation of a cell. Also included are:

(1) a vector comprising a proniferation of a cell. Also included are:

(1) a vector comprising a proliferation of the antisense

mucleic acid; (2) a host cell containing the vector; (3) an isolated

contisense mucleic acid; (4) an antibody capable of specifically binding

the polypeptide or its fragment whose expression is inhibited by the

antisense mucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

controliferation; (7) identifying a compound that influences the activity of

proliferation; (7) identifying a compound that inhibits proliferation; (8)

compound a gene required for cellular proliferation or the biological

controliferation, or that inhibits proliferation of an

corganism acts; (9) manufacturing an antibiotic; (10) profilling a

compound's activity; (11) a culture comprising strains in which the gene

product is overexpressed or underexpressed; (10) profilling a

compound's activity; (11) a culture comprising strains in which the gene

product is overexpressed or underexpressed; (12) determining the extent

conjugation of an organism. The antisense nucleic acids are useful for

the darrifying proteins or screening for homologous nucleic acids required

for cellular proliferation in cells other than S. aureus, S. typhimurium,

crequired for proliferation in cells other than S. aureus, S. typhimurium,

crequired for proliferation in cells other than S. aureus, S. typhimurium,

creduired for proliferation in cells other than S. aureus, S. typhimurium,

creduired for proliferation of the prinied specification, but was obtained

content of the larget product by the prinied specification, but was obtained
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                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                               invention relates to an isolated nucleic acid comprising any one of
                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.5%; Score 34; DB 6; Length 475; 57.1%; Pred. No. 3.8e+02; ive 0; Mismatches 3; Indels
                                                                  Ohlsen KL,
Forsyth RA,
                                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                           Claim 25; SEQ ID NO 57680; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. faecium protein sequence SEQ ID 6868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC97241 standard; protein; 478 AA
                                                                  Malone C,
Carr GJ,
06-MAR-2002; 2002US-0362699P.
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Best Local Similarity 57.1.
4; Conservative
                                (ELIT-) ELITRA PHARM INC.
                                                                  Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYWLSAW 101
                                                                                                                     WPI; 2003-029926/02
N-PSDB; ACA33626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 475 AA;
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                                                                    Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
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The invention relates to an isolated nucleic acid derived from
Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC ene of 10 fully defined sequences given in the (or comprising 40
c sequential nucleotides chosen from any of the nucleic acids, its
C complement or sequences hybridising to it). Also included are a
CC transcription regulatory element, a cell comprising the vector and a
CC transcription regulatory element, a cell comprising the vector and a
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CT he nucleic acids is useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection) and for screening drugs such as agonists and antagonists. The
CH concleic acid is useful for recombinant production of Candida albicans -
CC infection) and for screening drugs such as agonists and antagonists and avaccines containing the nucleic acid are useful for preventing or
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
Local Similarity 57.1%; Pred. No. 3.8e+02;
les 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus polypeptide SEQ ID NO 3112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP26968 standard; protein; 479 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 478 AA;
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Enterococcus faecium

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sequence (ABA90521) and related proceins (ABB33300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-06T-2001) which is available in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic
                                                                                                                                                                                               New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
                                                                                                                                                                                                                                                                                                                                                present invention is related to a Lactococcus lactis nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003
standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.5%; Score 34; DB 5; Length 490;
57.1%; Pred. No. 3.9e+02;
ive 0; Mismatches 3; Indels
                                                                                   Ehrlich SD;
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                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID NO 2091; 2504pp; French.
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                           (INRG ) INRA INST NAT RECH AGRONOMIQUE.
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                                                                                   Renault P,
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                                                                                   Sorokine A,
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                                                                                                                                          WPI; 2002-043418/06.
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                                                                                      Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2003
16-MAY-2002
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ABB55385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5403 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a Streptococcus that is particularly S. agalactiae and S. pyrogenes. Oli. A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meniatis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography.immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                         Masignani V, Margarit Y RosI, Grandi G, Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.5%; Score 34; DB 5; Length 479; 57.1%; Pred. No. 3.9e+02; tive 0; Mismatches 3; Indels
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                                                                             27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                        29-OCT-2001; 2001WO-GB004789.
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                                                                                                                                                                                               (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
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N-PSDB; ABN67599.
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Length 499; 3; Indels

Score 34; DB 7; Pred. No. 4e+02; 0; Mismatches

Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative

Sequence 499 AA;

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1 GYWXXXW 7

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acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO20017734 (published 18-OCT-2001) which is available in electronic format directly from WIPO at Etp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment opathological conditions resulting from bacterial infection.
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                             Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
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                                                                                                                                   Score 34; DB 5; Length 496;
Pred. No. 4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 23328; 455pp; English.
                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa polypeptide #6757.
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57.1%;
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98US-0094190P.
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                                                                                                                        Query Match
Best Local Similarity 57.1%,
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                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
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                                                                                                                Sequence 496 AA;
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21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00372851. 06-MAR-2002; 2002US-0362699P.

ELITRA PHARM INC

(ELIT-)

21-MAR-2002; 2002WO-US009107

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Burkholderia mallei.

WO200277183-A2.

03-OCT-2002

Protein encoded by Prokaryotic essential gene #7941.

(first entry)

19-JUN-2003

ABU22414;

ABU22414 standard; protein; 506 AA.

RESULT 15

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The first sense sequences given in the specification where expression of the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene present in a culture or collection of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 50338; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-029926/02.
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Wall D,
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segdata.uspto.gov/seguence.html

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proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                  Sequence 506 AA;
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89.5%; Score 34; DB 6; Length 506;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels

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Search completed: December 30, 2004, 13:07:56 Job time : 51.7358 secs

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Sequence 6868, Ap Sequence 19328, A Sequence 1937, A Sequence 19, Appli Sequence 10, Appli Sequence 11, Appl Sequence 6945, Ap Sequence 6945, Ap Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 279, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 179, Appl Sequence 1
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81, Appl
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18441, A
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                                                                                                              December 30, 2004, 12:59:07; Search time 16.1132 Seconds (without alignments) 28.810 Million cell updates/sec
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Compugen Ltd.
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US-09-792-616-3
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US-09-502-653-10
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US-09-107-532A-6945
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US-09-00-091-817
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                 version 5
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STRATE: Massachusetts
COUNTRY: USA
                                                                      19685, A
22994, A
5312, Ap
8752, Ap
4523, A
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US-09-621-976-7633
US-09-621-976-7239
US-09-252-991A-19685
US-09-252-991A-25994
US-09-489-039A-8752
US-09-270-767-45223
US-09-270-767-45223
US-09-252-991A-28537
US-09-794-517A-8
US-09-794-517A-8
US-09-794-813-8
US-09-794-813-8
US-09-794-813-8
US-09-794-813-8
US-09-680-860-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

COPERATING SYSTEM: «Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107, 532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085, 598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: 14 May 1998

ATTORNEY/AGENT INFORMATION:

NAME: ATIAIGLIO, Pamela Deneke

REGISTRATION NUMBER: 40, 489

REGISTRATION NUMBER: 40, 489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature;
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:
US-09-107-532A-6868
                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6868, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 478 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6868:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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### Sequence 18697, Application US/09252991A

### SEQUENCE INVERTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS

### TITLE OF INVERTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

### TITLE OF INVERTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

### CURRENT PILING DATE: 1999-02-18

### CURRENT PILING DATE: 1999-02-18

### PRIOR PELLING DATE: 1999-02-18

### PRIOR PELLING DATE: 1999-02-18

### PRIOR PELLING DATE: 1999-07-27

### NUMBER OF SEQ ID NOS: 33142

### IENGTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09792616.

Patent No. 6780587.

GENERAL INFORMATION:

APPLICANT: PAR International, Inc.

APPLICANT: DAIVERSTON: Mutations in a gene encoding an ABC transporter (MRP6) cauging TITLE OF INVENTION: Pseudoxanthoma Blasticum

TITLE OF INVENTION: Pseudoxanthoma Blasticum

TITLE OF INVENTION: DAIVERSTON: PSEUDOXANTHOMA BLASTICUM

CURRENT APPLICATION NUMBER: US/09/792,616

CURRENT FILLING DAIE: 2001-02-23

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09792616
Patent No. 6780587
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 543;
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Pred. No. 2.6e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        86.8%;
57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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US-09-792-616-9
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US-09-792-616-9
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US-09-792-616-3
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US-09-252-991A-23328

US-09-252-991A-23328

Sequence 23328, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICATION:

AUGINE AREPERBONE:

FILE REPERBENCE:

FURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PILICATION NUMBER: US 60/074,788

PRIOR PILICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR SEQ ID NOS: 33142

SEQ ID NO 23328
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              89.5%; Score 34; DB 4; Length 478; 57.1%; Pred. No. 1.6e+02; ive 0; Mismatches 3; Indels
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Pred. No. 2.6e+02;
0; Mismatches 3; Indels
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Pred. No. 1.6e+02;
0; Mismatches 3;
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23328
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57.1%;
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            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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RESULT 4

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FEACHLIA NO. 0.44/13/
AEPIERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15791
LENGTH: 274
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Pred. No. 2.1e+02;
0; Mismatches 3; Indels
                                                          84.2%; Score 32; DB 3; Length 252; 57.1%; Pred. No. 1.9e+02; tive 0; Mismatches 3; Indels
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CONTRIBUTION OF SERVICE STATE OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION O
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Patent No. 656606

GENERAL INFORMATION:
APPLICANT:
APPLICANT: Walker, Michael G.
APPLICANT: Volkmuth, Wayne
TITLE COF INVENTION: AQUAPORIN-8

TITLE REFERENCE: PC-0012 CIP
CURRENT FILING DATE: 2000-07-06
CURRENT FILING DATE: 2000-07-06

PRIOR PILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 12

LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 15791, Application US/09248796A; Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15791
                               Query Match
Best Local Similarity 57.1-
                                                                                                                                                                                                                                                                210 GYWEPAW 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 GYWDFHW 230
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US-09-502-653-10
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Patent No. 6605709
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PILING DATE: 2000-04-05
PRIOR PELING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7520
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US-09-502-653-10

Sequence 10, Application US/09502653

Patent No. 6331426

GENERAL INPORMATION:

APPLICANT: Schlein, Martin

APPLICANT: Schlein, Martin

APPLICANT: Schlein, Martin

APPLICANT: Schlein, Martin

APPLICANT: Schlein, Martin

APPLICANT: Schlein, Martin

APPLICANT: Schlein, Martin

APPLICANT: Schlein, Martin

APPLICANT: Schlein, Martin

SCHLENT: Bech, Lisbeth

FILE REFERENCE: 5481.200-US

CURRENT APPLICATION: NOVEL GALACTANASES

FILE REFERENCE: 5481.200-US

CURRENT APPLICATION NUMBER: PA 1999 00184

EARLIER APPLICATION NUMBER: PA 1999 00799

EARLIER PILING DATE: 1999-02-11

EARLIER PILING DATE: 1999-02-11

EARLIER PILING DATE: 1999-03-24

EARLIER PILING DATE: 1999-03-24

EARLIER PILING DATE: 1999-03-24

EARLIER PILING DATE: 1999-06-10

NUMBER: OF SEQ ID NOS: 52

LENGTWARE: FEBLESCQ for Windows Version 3.0

SEQ ID NO 10

LENGTH: DATE: DATE

LENGTH: 252

TAVED: NON 10
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                                                                                                                                                                                                                                 Best Local Similarity 57.1
Matches 4; Conservative
                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-09-792-616-3
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Best Local Similarity
Matches 4; Conserv
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US-09-543-681A-7620
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                               LENGTH: 1503
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SEQ ID NO 3
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE DE INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26841
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 84.2%; Score 32; DB 4; Length 339; Best Local Similarity 57.1%; Pred. No. 2.5e+02; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
CONTRY: United States of America
ZIP: 94306-186
ZIP: 94306-186
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
COMPUTER: PC
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYPEPTIDES BINDING ANTI-
CRYPTOSPORIDIUM ANTIBODIES, DNA
AND RNA ENCODING THEM, HYBRID
VECTOR AND TRANSFORMED HOST AND
METHODS FOR IMMUNOTHERAPY AND
DIAGNOSIS AND KIT
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J. Sequence 6, Application US/08415751

J. Patent No. 5643772

J. GERREAL INFORMATION:

RAPLICANT: BEECH, JAMES

APPLICANT: BEECH, JAMES

APPLICANT: BEECH, JAMES

APPLICANT: GUT, JIRI

TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, D

TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, D

TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRID

TITLE OF INVENTION: WECTOR AND TRANSPORMED HOST A

TITLE OF INVENTION: WETHORS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS AND KIT

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: PHILLIPS, MOORE, LEMPIO & FINLEY

STATE: Palo Alto

COTTY: Palo Alto

STATE: California
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REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)
                                                                              Sequence 26841, Application US/09252991A Patent No. 6551795
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APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: MAY 29, 1992
ATTORNEY AGENT INFORMATION:
NAME: Hana Dolezalova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 GYWGGYW 267
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                                                         JS-09-252-991A-26841
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Pred. No. 2.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                            APPLICANT: Abbort Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Ananda E. Y.
APPLICANT: Leonard, Ananda E. Y.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Huang, Yung-Sheng
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: Kirchner, Stephen J.
APPLICANT: STEPHENCE: 6407.US.01
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT APPLICATION NUMBER: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ADDOCT LEGISTICS
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Heang, Yung-Sheng
APPLICANT: Heang, Yung-Sheng
APPLICANT: Hearing, Yung-Sheng
APPLICANT: Bereira, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 640° US. P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT PILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 09/624,670
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/379,095
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FRASEQ FOR WINDOWS Version 4.0
                                                                                                                                       US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 1, 6403349
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/09903456; Patent No. 6677145; Patent No. 1677145; APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Caenorhabditis elegans
US-09-145-828A-11
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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84 GYWPITW 90
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US-09-903-456-18
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LENGTH: 278
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LENGTH: 278
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Gaps

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Sequence 15189, Application US/09248796A

Patent No. 6747137

SEGUENCE 15189, Application US/09248796A

SEQUENCE 15189, Application US/09248796A

SEQUENCE 15189, Application

SEQUENCE 15189

SEQUENCE 16718710N

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PELING DATE: 1999-02-12

CURRENT FILING DATE: 1999-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER: OF SEQ ID NOS: 28208

SEQ ID NO 15188

LENGTH: 367
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                                                                                                                                                                                                                                                                                     ) NAME/KEY: Positions coded by nonsense codons are; NAME/KEY: identified as Xaa. US-08-415-751-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 30, 2004, 13:19:22 Job time : 18.1132 secs
             TELEPHONE: (415) 324-1677
TELEPHONE: (415) 324-1678
INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORIGINAL SOURCE:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 57.1
Matches 4, Conservative
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US-09-248-796A-15188
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Sequence 308836, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Los Novalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 308836
LENGTH: 58
US-10-046-922-34

US-10-046-922-35

US-10-425-115-287762

US-10-425-115-273234

US-09-910-483-5

US-09-910-483-5

US-09-910-483-17

US-09-910-483-25

US-09-910-483-25

US-09-910-483-37

US-09-910-483-37

US-09-910-483-37

US-09-910-483-37

US-09-910-483-37

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US-09-910-483-37

US-10-160-232-96

US-11-160-232-96

US-11-160-232-96

US-11-160-232-96

US-11-156-115-34595

US-11-156-115-34695

US-11-156-115-34695

US-11-156-115-34695

US-11-156-115-34695

US-11-156-115-34695

US-11-156-115-34695

US-11-156-115-34695

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US-11-450-022-4

US-11-450-022-5

US-11-431-7478-7
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US-10-425-115-308836
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US-10-437-963-176036
; Sequence 176036, Application US/10437963
; Publication No. US20040123343A1
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57.1%;
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Best Local Similarity
Matches 4; Conserv
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ORGANISM: Zea mays
   GYWGASW
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       49
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Sequence 49513, A
Sequence 23291, A
Sequence 52805, A
Sequence 13733, A
Sequence 68169, A
Sequence 68169, A
Sequence 87, Appl
Sequence 87, Appl
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                                                                                                                   December 30, 2004, 13:08:04; Search time 52.1698 Seconds (without alignments) 48.267 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
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| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
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| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
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| Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.ppp:*
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| Cgn2_6/ptodata/1/pubpaa/US0_PUB.ppp:*
| Cgn2_6/p
                     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-437-96--176036
US-10-091-007-88
US-10-282-122A-49513
US-10-282-122A-65258
US-10-282-122A-6528
US-10-282-122A-6528
US-10-282-122A-5680
US-10-282-122A-5080
US-10-282-122A-50338
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                                                                                                                                                                                                                                                                                                           1599051 segs, 359727711 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                     Copyright
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                                                                                                                                                                                        Title:
Perfect score:
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Length 58 Indels

Sequence 9632, Ap Sequence 19811, A Sequence 16537, A Sequence 199114,

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Sequence 3 Sequence 3 Sequence 5

117, Appl 22, Appl 22, Appl 33, Appl 31, Appl 41, Appl 41, Appl 43, Appl 86, Appl 64263, A

Sequence Sequence

Sequence Sequence Sequence

Sequence 3 Sequence 3 Sequence 8

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Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

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Sequence 23291, Application US/10369493

Sequence 23291, Application US/10369493

Sequence 23291, Application US/10369493

Sequence 23291, Application US/10369493

GENERAL INFORMATION:
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Marieng
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-21

SEQ ID NO 23291

LENGTH: 469
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: LITTRA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 00/191,078

PRIOR APPLICATION NUMBER: 60/206,846

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 2001-02-03

PRIOR PRIOR PRIOR DATE: 2001-02-06

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                                                                         Trawick, John
Carr, Grant
Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Bacillus subtilis
US-10-369-493-23291
Zyskind, Judith
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Best Local Similarity 57.1
Matches 4; Conservative
                                      Wall, Daniel
Trawick, Joh
                                                                                                                                                                                                           Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 GYWVSAW 92
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                                               Lardant: Li, Pind

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPRENCE: 38-21(51221)B

CURRENT APPLICATION NUMBER: 18/10/437,963

CURRENT FILING DATE: 2003-05-14

SEQ ID NOS: 204966

LENGTH: 72

TYPE: WITH TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES TO THE TABLES T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_73824C.1.pep
US-10-437-963-176036
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Sequence 88, Application US/10091007

Sequence 88, Application US/10091007

Publication No. US20030170782A1

GENERAL INFORMATION:

APPLICANT: Microbial Technics limited

APPLICANT: Le Page, Richard W F

APPLICANT: Hanniffy, Sean B

TITLE OF INVENTION: Proteins

TILE REFERENCE: PWC/P21978W0

CURRENT APPLICATION WUMBER: US/10/091,007

CURRENT FILING DATE: 1999-09-07

NUMBER OF SEQ ID NOS: 276

SOFTWARE: PatentIn version 3.0

SEQ ID NO 88
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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; ORGANISM: Streptococcus agalactiae
US-10-091-007-88
                              APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Matches 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GYWSSHW 40
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GENERAL INFORMATION:
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95 GYWLSAW 101
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US-10-369-493-13733
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### AFFLICANTION: Identification of Essential Genes in Microorganisms

### FILE REPERENCE: ELITRA.034A

### CURRENT APPLICATION NUMBER: US/10/282,122A

### CURRENT PILING DATE: 2000-03-21

### PRIOR FILING DATE: 2000-03-21

### PRIOR FILING DATE: 2000-05-23

### PRIOR FILING DATE: 2000-05-23

### PRIOR FILING DATE: 2000-05-23

### PRIOR PILING DATE: 2000-05-26

### PRIOR FILING DATE: 2000-05-06

### PRIOR FILING DATE: 2000-05-06

### PRIOR FILING DATE: 2000-09-06

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### PRIOR FILING DATE: 2000-09-09

### PRIOR FILING DATE: 2000-10-29

### PRIOR FILING DATE: 2000-11-27

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### PRIOR PILING DATE: 2001-12-24
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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89.5%; Score 34; DB 14; Length 469; 57.1%; Pred. No. 5.8e+02; ive 0; Mismatches 3; Indels
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US-10-282-122A-52805
; Sequence 52805, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Sequence 66258, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66258
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Wall, Daniel
Trawick, John
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Yamamoto, Robert
Forsyth, R.
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                                                            4; Conservative
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Best Local Similarity
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US-10-282-122A-66258
   Query Match
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HAPLICANY Zamado, Carlos

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## APPLICANI: AU, H.

## CURRENT APPLICANION: Identification of Essential Genes in Microorganisms

## CURRENT APPLICATION NUMBER: US/10/282,122A

## CURRENT FILING DATE: 2003-02-20

## PRIOR APPLICATION NUMBER: 60/191,078

## PRIOR PILING DATE: 2000-05-23

## PRIOR PELING DATE: 2000-05-23

## PRIOR PELING DATE: 2000-05-26

## PRIOR PELING DATE: 2000-05-26

## PRIOR PELING DATE: 2000-05-26

## PRIOR PELING DATE: 2000-05-06

## PRIOR PELING DATE: 2000-09-09

## PRIOR PELING DATE: 2000-09-09

## PRIOR PELING DATE: 2000-10-23

## PRIOR PELING DATE: 2000-10-23

## PRIOR PELING DATE: 2000-10-23

## PRIOR PELING DATE: 2000-11-27

## PRIOR PELING DATE: 2000-12-22

## PRIOR PELING DATE: 2000-12-26

## PRIOR PELING DATE: 2001-12-20

## PRIOR PELING DATE: 2001-02-09

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57680, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                TYPE: PRT CAGANISM: Pseudomonas fluorescens US-10-369-493-13733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57680
                                                                                                                                                                       89.5%;
57.1%;
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APPLICANT: Aamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Wall, Daniel
Trawick, John
Carr, Grant
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Forsyth, R.
Xu, H.
                                                                                                                                                                Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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US-10-282-122A-57680
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LENGTH: 475
LENGTH: 475
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; ORGANISM: Artificial Sequence
; PEATURE:
; CTHER INV-TC
US-09-894-018-87
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Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                        22 GYWQATW 28
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US-10-046-922-34
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                                                                      APPLICANT: AU, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
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PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 50338
LENGTH: 506
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APPLICANT: Sette, Alessandro
APPLICANT: Chestmut, Robert
APPLICANT: Chestmut, Robert
APPLICANT: Chestmut, Brian
APPLICANT: Baker, Denisw
APPLICANT: Baker, Denisw
APPLICANT: Baker, Denisw
APPLICANT: Baker, Denisw
APPLICANT: Bewan, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-2003.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
CRRIOR APPLICATION NUMBER: US 60/29568
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
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PRIOR APPLICATION NUMBER: US 60/284,221
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Sequence 87, Application US/09894018
Patent No. US20020119127A1
FREENT NO. US20020119127A1
FREENT NFORMATION:
APPLICANT: EPIMMUNE, Inc.
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  Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 57.1
Matches 4; Conservative
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LENGTH: 585
TYPE: PRT
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APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Newman, Mark
APPLICANT: Brown, Javid
TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
FILE REFERENCE: 2060.0320004
CURRENT APPLICATION NUMBER: US/10/474,960A
CURRENT FILING DATE: 2003-10-16
PRIOR PILING DATE: 2002-03-28
PRIOR PLING DATE: 2002-03-28
PRIOR PLING DATE: 2001-06-27
PRIOR PLING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 87
LENGTH: 585
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Sequence 34, Application US/10046922;
Publication No. US20020164667A1;
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari;
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VECFR-3 INHIBITOR MATERIALS AND METHODS;
TITLE OF INVENTION: USCFR-3 INHIBITOR MATERIALS AND METHODS;
CURRENT APPLICATION UNDBER: US/10/046,922;
CURRENT FILING DATE: 2002-01-15;
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 585;
Score 34; DB 9; Length 585;
Pred. No. 6.9e+02;
0; Mismatches 3; Indels
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57.1%; Pred. No. 6.9e+02;
ive 0; Mismatches 3.
                                                                                                                                                                                                                                                                   Sequence 87, Application US/10474960A Publication No. US20040248113A1 GENERAL INFORMATION:
APPLICANT: Sette, Alessandro APPLICANT: Cheenut, Robert
  h 89.5%;
Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: isolated peptide
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US-10-046-922-35

i Sequence 35, Application US/10046922

sequence 35, Application US/10046922

publication No. US20020164667A1

GENERAL INFORMATION:

APPLICAMY: Altalo, Kari

APPLICAMY: Kubo, Hajime

TITLE OF INVENTION: VEGER-3 INHIBITOR MATERIALS AND METHODS

TITLE OF INVENTION: WEGER-3 US/10/046,922

CURRENT APPLICATION NUMBER: US/10/046,922

CURRENT FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 80

SEQ ID NO 35

LENGTH: 10
                                                                                                                                                                                           Query Match 86.8%; Score 33; DB 13; Length 10; Best Local Similarity 57.1%; Pred. No. 42; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 86.8%; Score 33; DB 13; Length 10; Best Local Similarity 57.1%; Pred. No. 42; Matches 4; Conservative 0; Mismatches 3; Indels
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35
                                                                                                                                                                                                                                                                                  1 GYWXXXW 7
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Search completed: December 30, 2004, 13:50:02 Job time : 53.1698 secs

2 GYWLTIW

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

December 30, 2004, 12:58:17; Search time 8.0566 Seconds (without alignments) 83.598 Million cell updates/sec Run on:

US-10-046-922-67 38 1 GYWXXXW 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de			SUMMARIES	
Regult No.	Score	Query	, Length	DB	ID	Description
1	34	89.5	!	7	T03190	hypothetical prote
~	34	89.5		~	S12193	
٣	34	89.	m	~	T37139	
4	34	3.68		~	D70048	ABC transporter (a
'n	34	89.		~	E83497	probable amino aci
9	34	89.5	٠.	~	T46745	arginine/ornithine
7	34	89.5	. `	~	JH0110	arginine/ornithine
œ	34	89.	٠.	~	C86879	arginine/ornitine
σ	34	3.68		~	G86878	arginine/ornitine
2		86.8		7	C34903	Ig heavy chain pre
1	33	86.8		7	S73905	CDPdiacylglycerol-
12		86.8		~	A69843	hypothetical prote
13	33	86.8		~	G72215	oligopeptide ABC t
14	33	86.8		~	AE2047	hypothetical prote
15	33	86.8		7	C95307	probable transport
16	33	86.8		~	C95282	probable ABC trans
17	33	86.8		7	A13201	hypothetical prote
18	33	86.8		~	E83268	Ω
19	33	86.8		7	T15414	hypothetical prote
20	33	86.8		~	B95952	a)
21	33	9.98		~	AC2392	hypothetical prote
22	33	86.6		~	AH2975	
23	33	86.8		ď	C98307	ophA protein [impo
24	33	86.		~	T15413	hypothetical prote
52	33	86.8		~	T31037	
56	33	86.8	3 1502	~	T42216	α
27	32	84.		~	29	-
28	32	•	2 83	~	σ	hypothetical prote
29	32	84.	2 187	~	G83047	

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Query Match 89.5%; Score 34; DB 2; Length 108; Best Local Similarity 57.1%; Pred. No. 21; Matches 4; Conservative 0; Mismatches 3; Indels

A; Genome: plasmid pTF1

1 GYWXXXW 7

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	nyponnerical proce probable mccF prot	aquaporin 8 - mous	aquaporin 8 - rat	phosphatidate cyti	phosphatidate cyti	probable sugar ABC	protein F41H10.7 (	hypothetical prote	siderophore/Surfac	conserved hypothet	probable secreted	oligopeptide trans	probable ABC trans	hypothetical prote
S76385	E75325	JC5806	JC5622	F83188	JC4832	H95869	E88690	C82611	H97146	AB0301	T35164	877572	G95389	B86233
~ ~	v (4	N	~	~	~	~	N	~	~	N	~	~	~	0
218	257	261	263	271	271	282	286	344	447	448	466	519	536	631
84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2		84.2	84.2
32	3 2	32	32	32	32	32	32	32	32	32	32	32	32	32
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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C, Accession: T01100
R; Itadani, H.; Makasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.
Plant Cell Physiol. 35, 1239-1244, 1994
A; Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existence A; Reference number: Z14841; MUID:95211382; PMID:7545979
A, Accession: T03100
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPROT:035302; EMBL:D32052; NID:9769704; PIDN:BAA06811.1; PID:9769703; A; Experimental source: cultivar Nipponbare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypotherical protein 4 - Thiobacillus ferrooxidans plasmid pTF1

C.Species: Thiobacillus ferrooxidans

C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C.Accession: S12193

A.Trle: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans is A.Reference number: S12188; MUID:91125140; PMID:2280689

A.Reference number: S12188; MUID:91125140; PMID:2280689

A.Reference preliminary; translation not shown

A.Molecule type: DNA

A.Residues: 1-108 <-DRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P20088; EMBL:X52699; NID:g48158; PIDN:CAA36930.1; PID:g48164
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
hypothetical protein 72B - rice mitochondrion
C;Species: mitochondrion Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Genome: mitochondrion
C;Keywords: mitochondrion
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M.J.; Br;
K.; Lim,
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A;Reference number: A82950; WUID:20437337; PMID:10984043
A;Accession: E83497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:0914E4; GB:AE004549; GB:AE004091; NID:g9947110; PIDN:AAG0458:
A;Experimental source: strain PAO1
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C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: JH0110; A8299
C;Accession: JH0110; A8299
R;Luethi, B.; Baur, H.; Gamper, M.; Brunner, F.; Villeval, D.; Mercenier, A.; Haas, D.
Gene 87, 37-43, 1990
A;Title: The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa cont;
A;Reference number: JH0110; MUID:90236296; PMID:2158926
A;Accession: JH0110
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Gene: arcD
Symutonic necessary for arginine transport; involved in ornithine-arginine exchange
A; Pathway: arginine catabolism
C; Superfamily: L-lysine transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, C. Bacteriol. 180, 415-4159, 1998
A;Title: Structural and functional analysis of the gene cluster encoding the enzymes of A;Reference number: 223141; MUID:98361904; PMID:9696763
                                                                            robable amino acid permease PA1194 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                          C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Datession: B83497
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T46745
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
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Pred. No. 81;
0; Mismatches
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Pred. No. 81;
0; Mismatches
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C;Superfamily: L-lysine transport protein
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Similarity 57.1%;
4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYWLSAW 100
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Best Local Similarity
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A; Residues: 1-472 <STO>
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DECURE 4

DECURE 5

DECURE 6

DECISION 19

ABC transporter (amino acid permease) homolog yv8H - Bacillus subtilis

CiSpecies: Bacillus subtilis

CiSpecies: Bacillus subtilis

CiBate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

CiBate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

CiBate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

CiBate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

CiBate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

CiBate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

CiBate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jul-2004

A: Ehrlich, S.D.; Emmerson, P.T.; Entian, M.D.; Erington, J.; Fabret, C.; Ferrari, E.

Naturors: 300, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Hanatt, A.; Halbert, H.; Marcho, A.; Liu, H.; Masuda, S.; Maueell X.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schliech, S.; Schroeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tompeter, P.; Tomp
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A;Cross-references: UNIPROT:Q9S1R7; EMBL:AL109972; PIDN:CAB53264.1; GSPDB:GN00070; SCOED
A;Cross-references: uniprot: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCJ9A.03c
C;Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c
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                                                                                                                                                                               hypothetical protein SCJ9A.03c - Streptomyces coelicolor
hypothetical protein SCJ9A.03c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37139
R;Harris, D:; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A;Reference number: Z21622
A;Reference number: Z21622
A;Reference number: Z21622
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.5%; Score 34; DB 2; Length 345; 57.1%; Pred. No. 61;
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C; Genetics:
A; Gene: yvek
C; Superfamily: L-lysine transport protein
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GYWRSSW 95
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Matches 4; Conserv
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Genetics:

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A;Cross-references: UNIPROT:Q9CE19; GB:AE005176; PID:g12725079; PIDN:AAK06129.1; GSPDB:GhA;Experimental source: strain IL1403
C;Genetics:
A;Gene: arcD2
C;Superfamily: L-lysine transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use heavy chain precursor V region (5-27) - mouse
CiSpecies: Mus musculus (house mouse)
CiAccession: C34903
Ribedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. (Chem. 265, 133-138, 1990
J. Biol. (Chem. 265, 133-138, 1990
J. Fitle: Active site structure and antigen binding properties of idiotypically cross-reach, Ricession: C34903
A.Fitle: Active site structure and antigen binding properties of idiotypically cross-reach, Ricession: C34903
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-142 - ABED>
CiSuperfamily: immunoglobulin V region; immunoglobulin homology
CiKeywords: heterotetramer; immunoglobulin
F;34-119/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-227 cHIM>
A; Cross-references: UNIPROT: P75520; EMBL: AE000057; GB: U00089; NID: g1674279; PIDN: AAB9622: A; Notes: references: UNIPROT: P75520; EMBL: AE000089; NID: g1674279; PIDN: AAB9622: A; Notes: The nucleotide sequence was submitted to the EMBL Data Library, November 1996
A; Genetics: A; Genetics: A; Genetic code: SGC3
A; Genetic code: SGC3
C; Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
C; Keywords: transferase
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                                                                                                                                                                                         89.5%; Score 34; DB nilarity 57.1%; Pred. No. 85; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                93 GYWISAW 99
                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserv
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUID:21235186; PMID:11337471
A; Residues: 1482 <-LUE>
A; Residues: 1482 <-LUE>
A; Cross-references: UNIPROT:P18275; GB:M33223; NID:g151030; PIDN:AAA25719.1; PID:g151031
A; Cross-references: UNIPROT:P18275; GB:M33223; NID:g151030; PIDN:AAA25719.1; PID:g151031
A; Experimental source: strain PAOI
A; Note: the gene encoding this protein is located upstream of the arcABC genes which ence R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Rstover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic patho A; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                            A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-482 <STO>
A, Cross-references: GB: AE004930; GB: AE004091; NID: 99951472; PIDN: AAG08555.1; GSPDB: GN001
A, Experimental source: strain PAO1
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A,Reaidues: 1-490 <STO>
A,Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:C
A,Experimental Bource: strain IL1403
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Pred. No. 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2;
Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: arcD; PA5170
C;Superfamily: L-lysine transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: arcDl
C;Superfamily: L-lysine transport protein
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ilarity 57.1%;
Conservative
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Best Local Similarity 57.1
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Best Local Similarity
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Genetics:

RESULT 9

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C;Accession: AE2047
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q8YVP3; GB:BA000019; PIDN:BAB73630.1; PID:g17131021; GSPDB:GP
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a111931
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
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K; Barnett, M.J.; Fisher, K.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse

K; Barnett, M.J.; Fisher, K.F.; Jones, T.; Komp, C.; Abola, A.P.; Wells, D.H.; Yeh, K.C.;

K; Karing, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot:

A; Reference number: A95262; MUID:21396509; PMID:11481432
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A;Nolecule trype: DNA
A;Residues: 1-441 < kUNA
A;Residues: 1-441 < kUNA
A;Residues: 1-441 < kUNA
A;Residues: 1-441 < kUNA
A;Residues: 1-441 < kUNA
A;Residues: 1-441 < kUNA
A;Residues: 1-471 < kuna
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A;
                                                                                                                                                                               hypothetical protein all1931 [imported] - Nostoc sp. (strain PCC 7120)
C.Species Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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Pred. No. 1.1e+02;
0; Mismatches 3;
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Pred. No. 94;
0; Mismatches
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C;Superfamily: L-lysine transport protein
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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Matches
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A69843
hypothetical protein yjbA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69843
R;Kunst, F:, Ogaswara, N:; Moszer, I:; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hoadono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Ladinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rock, M.; Sadaie, V.; Sato, T.; Sachoni,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sckiguchi, J.; Sekowska, A.; Serol
Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, K.; Yata, Yata, K.; Yata, Yata, Yata, Yata, Yata, Yata
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72215
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-289 <ARN>
A;Cross-references: UNIPROT:09X270; GB:AE001813; GB:AE000512; NID:g4982321; PIDN:AAD3681
A;Experimental source: strain MSB8
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A,Cross-references: UNIPROT:031597; GB:299110; GB:AL009126; NID:g2633472; PIDN:CAB12998.
A,Experimental source: strain 168
C,Genetics:
A,Gene: yjbA
C,Superfamily: Bacillus subtilis hypothetical protein yjbA
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Oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)

Cispecies: Thermotoga maritima
Cibate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
CiAccession: G72215
Rivelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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Q6hdl5 cenococcus
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Q73dl5 bacillus ce
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Q7zj17 human immun
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Q7uv7 prochloroco
Q6nf17 corynebacte
Cae50615 corynebac
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P75520 mycoplasma
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EMBL; D32052; BAA06811.1; -...
Gramene; Q35302; -...

GO; GO:0005739; C:mitochondrion; IEA.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Pred. No. 87;
0; Mismatches
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"Frequent detection of escape from cytotoxic T-lymphocyte recognition in perinatal human immunodeficiency virus (HIV) type I transmission: the ariel project for the prevention of transmission of HIV from mother to infant.";
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MEDLINE=97369814; PubMed=9226255;
Duwat P., Cochu A., Ehrlich S.D., Gruss A.;
"Characterization of Lactococcus lactis UV-sensitive mutants obtained
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J., Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M., Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
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57.1%; Pred. No. 2.5e+02;
tive 0; Mismatches 3; Indels
   Indels
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236 AA; 27062 MW; 24D6BB0409AB0BBB CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Arginine/ornithine antiporter homolog ArcD (Fragment).
                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF121641, AAD29013.1;

EMBL, AF121641, AAD29013.1;

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004523; F:nibonuclease H activity; IEA.

InterPro; IPR002156; RNaseH.

InterPro; IPR010659; RVT_connect.

InterPro; IPR010661; RVT_thumb.
                                                                                                                                                                                                                                                                             236 AA.
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   Mismatches
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Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
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Best Local Similarity 57.1.
4; Conservative
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                                                                                                                   7 GYWTLAW 13
                                                           1 GYWXXXW 7
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Walker B.D.;
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01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 33020;
MEDLINE=91125140; PubMed=2280689;
Drolet M., Zanga P., Lau P.C.K.;
"The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
Mol. Microbiol. 4:1381-1391(1990).
                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales; Acidithiobacillaceae; Acidithiobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
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                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypotherical 12.3 kDa protein in mobl 3'region (ORF 4).
Thiobacillus ferrooxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52699; CAA36930.1; -.
PIR; S12193; S12193.
Hypothetical protein; Plasmid.
SEQUENCE 108 AA; 12335 MW; A8E67717C109A57E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 AA; 14024 MW; EE0F4A997FCA8CD8 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible Adenoviral fiber protein (Repeat/shaf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 AA.
                               108 AA
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                            PRT;
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EMBL; BX572092; CAE19526.1; -.
Complete proteome.
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Best Local Similarity 57.11,
Best A; Conservative
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                               STANDARD;
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Darbow, Vallenet D., Fonknechten N., Kreimeyer A., Oztas S., Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P., Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.; "Unique features revealed by the genome sequence of Acinetobacter sp. ADPI, a versatile and naturally transformation competent bacterium."; Nucleic Acids Res. 0:0-0(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Chalila G.L., Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H., Harris D.B., Quail M.A., Kieser H., Gronn A., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Huang C.H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Mature 417.141-147(2002).
EMBL; AL999104; CAB53264.1; -.
PIR; T37139; T37139.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.5%; Score 34; DB 2; Length 333; 57.1%; Pred. No. 3.5e+02; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
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SEQUENCE 345 AA; 36929 MW; 23643009936285B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                333 AA; 36530 MW; 7C887F5127A40682 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ©9S1R7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SCO0224.
OrderedLocusNames=SCO2224; ORFNames=SCJ9A.03C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 AA.
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                                                                                                                                                                                                                                                                                                                    EMBL; CR543861; CAG70223.1; ...
InterPro; IPR002657; BilAc/Na_symport.
Pfam; PF01758; SBF; 1.
Complete proteome:
SEQUENCE 333 AA; 36530 MW; 7C887F5
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                        Moraxellaceae; Acinetobacter
NCBI_TaxID=62977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 GYWASRW 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                   SEQUENCE FROM N.A.
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Q9KGV3;
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Matches
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                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acida Res. 30:3927-3935(2002).
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-1- SIMILARITY: BELONGS TO THE ABC-3 SUBFAMILY OF INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6F6U4 PRELIMINARY, PRT; 333 AA.
Q6F6U4;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transporter; putative sodium/bile acid transporter family
                     EMBL; U81991; AAC45504.1; -. CONTROL OF TRANSON OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONT
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                                                                                                                                                                                                                                                                                           Score 34; DB 2; Length 253; Pred. No. 2.7e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Transmembrane; Transport.
SEQUENCE 294 AA; 31323 MW; F75E50F22EA4071A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-HTE831;
MEDLINE-22220767; PubMed-12235376;
Takami H., Takaki Y., Uchiyama I.;
J. Bacteriol. 179:4473-4479(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acinetobacter sp. (strain ADP1).
                                                                                                                                                                                                                                                                                           89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.1%;
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OrderedLocusNames=ACIAD3583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=OB0434;
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 GYWLSAW 99
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ID Q6F6
D7 O5-J
DT O5-J
DT D5-J
DE Puta
DE Prot
GN Orde

us-10-046-922-67.rup

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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin B., Tice H.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AE017355; AAT62417.1; -.
InterPro; IPR004293; AA/rel_permeasel.
InterPro; IPR004841; Permease_region.
Pransmembrane; Transport.
SEQUENCE 465 AA; 50153 MW; 534F03BC0A379E04 CRC64;
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchrock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AE017225, AAT5224-1; -.

Interpro; IPR004841; Permease1.

Interpro; IPR004841; Permease region.

Pfam; PF00324; AA_permease; 1.

Transmembrane; Transport.

SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;
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                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Probable arginine/ornithine antiporter protein.
Name=arch; ORFNames=BT9727 0540;
Bacillus thuringiensis Bacillales; Bacillaceae; Bacillus;
Bacillus thuringiensis serovar konkukian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Amino acid permease family protein.
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                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                94 GYWLSSW 100
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   1 GYWXXXW 7
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Q6HNI4;
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Matches
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                                                                                                                                                                   RESULT 11
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STRAIN=ATCC 23279;
MEDLINE=22519909; PubMed=12631210;
Divol B., Tonon T., Morichon S., Gindreau E., Lonvaud-Funel A.;
"Molecular characterization of Oenococcus oeni genes encoding proteins
                                                                                                                              Name=arcD1;
Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
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Chou L.-S., Weimer B., Xie Y.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF282249; AAF86987.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
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J. Appl. Microbiol. 94:738-746(2003).

EMBL; AF541253; AA08332.1;

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:000579; F:amino acid-polyamine transporter activity; IEA.

GO; GO:0006865; P:amino acid-polyamine transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR002233; AA/rel_permease1.

InterPro; IPR004841; Permease_region.

Pfam; PF00324; AA, Dermease_region.

Pfam; PF00324; AA, Dermease.

Transmembrane; Transport.
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InterPro; IPR004841; Permease_region.
Pfam, PF00324; AA_permease; 1.
Transmembrane; Transport.
SEQUENCE 459 AA; 49146 MW; 9718F27B7E937242 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
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Bacteria; Firmicutes; Lactobacillales; Oenococcus.
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Best A; Conservative
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Length 465;

89.5%; Score 34; DB 2; Length 465 57.1%; Pred. No. 4.78+02; ive 0; Mismatches 3; Indels

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465 AA; 50040 MW; 9750B5D1019142F2 CRC64;
           Query Match
Best Local Similarity 57.1-
                                                                                                                                                                                                                                                      Bacillus anthracis.
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MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhatracharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Golteman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE017000; AAP07646.1; -. GMBL. AE017000; AAP07646.1; -. GC; GO:0016021; C:integral to membrane; IEA. GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA. GO; GO:0006810; P:transport; IEA. GO; GO:0006810; P:transport; IEA. InterPro; IPR002293; AA/xel_permeasel. InterPro; IPR004841; Permease_region. PF00324; AA_permease_region. Pfam; PF00324; AA_permease; I. Transmembrane; Transport.
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OrderedLocusNames=BCE0697;
Bacillus Cetaeus (strain ATCC 10987).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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InterPro; IPR004641; Permease_region.
Pfam; PF00324; AA_permease; T.
Complete proteome; Transmembrane; Transport.
SEQUENCE 465 AA; 50193 MW; C18384E10EEC639D CRC64;
                                                                                                  Last sequence update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Arginine/ornithine antiporter.
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 GYWAANW 102
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Q73DL5;
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X MEDLINE=22608114; PubMed=12721629; DOI=10.1038/nature01586;

Read T.D., Peterson S.N., Toursase N.J., Baillie L.W., Paulsen I.T.,

Nelson K.B., Tettellin H., Fouts D.E., Eisen J.A., Gill S.R.,

A Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.C.,

A Rolonay N.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Berton W.C., Peterson J.D., Pop M., Matkins K.L., Nierman W.C.,

A Barton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

A Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

A Hanna P.C., Kolstoe A.-B., Praser C.M.;

T.The genome sequence of Bacillus anthracis Ames and comparison to
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STRAIN-FAMES / isolate 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
"Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AR017026; AAP24646.1;
EMBL; AE017334; AAT29732.1;
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GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
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Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches '' 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=1392;
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                                                                                                                                                                                                       081V71; Q6KX71;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 28, Last annotation update)
Amino acid permease family protein.
OrderedLocusNames=BA0629; ORFNames=GBAA0629;
                                                                                                                                                                                465 AA
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InterPro; IPR004841; Permease_region.
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Transmembrane; Transport.
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96 GYWAANW 102
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(LUDW-) LUDWIG INST CANCER RES (LICN ) LICENTIA LTD.
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Misc-difference 4.
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Abp53965 VEGFR-3 b
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                                        December 29, 2004, 22:08:20 ; Search time 148 Seconds (without alignments) 19.391 Million cell updates/sec
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Aby24235
Aar32766
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Aar97730
Aay02418
Aay02418
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Compugen Ltd.
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	Adk11160	ADK11160	~	8	64.1	25	<u>س</u>
Somatosta	Adh68008	ADH68008	7	80	64.1	52	42
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Somatosta	Aaw97185	AAW97185	7	8	64.1	52	
Somatosta	Aaw45740	AAW45740	7	80	64.1	52	6
Somatosta	Aay18229	AAY18229	7	Φ	64.1	22	80
Somatosta	Aay22044	AAY22044	~	<b>6</b> 0	64.1	22	7
Somatosta	Aaw51865	AAW51865	~	80	64.1	22	9
Somatosta	Aaw18454	AAW18454	7	80	64.1	52	D.
Somatosta	Aar85570	AAR85570	~	80	64.1	25	
Somatosta	Aar76205	AAR76205	~	80	64.1	25	m
Somatosta	Aar76207	AAR76207	~	80	64.1	52	0
Somatosta	Aar56781	AAR56781	~	80	64.1	25	-
Somatosta	Aar42653	AAR42653	7	80	64.1	22	0
Somatosta	Aar31511	AAR31511	~	Φ)	64.1	52	6
Somatosta	Aar31513	AAR31513	0	80	64.1	25	8
Somatosta	Aar41502	AAR41502	N	80	64.1	25	7
Octapepti	Aar40822	AAR40822	~	<b>6</b> 0	64.1	25	w

#### ALIGNMENTS

Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypothensive, antidiabetic; vulnerary; call surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor. VEGFR-3 binding peptide SEQ ID NO:67. 7 A. ABP53964 standard; peptide; (first entry)

/note= "X is any amino acid" Location/Qualifiers

Kubo H;

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

Claim 21; Page 81; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive,

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antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence present invention
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antidiabetic and vulnerary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, spancres, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, brinnic hepatitis, haemangiomas and diabetes. The present sequence present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                     82.1%; Score 32; DB 5; Length 7; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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'note= "X is any amino acid"
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the treatment
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                                                           Gaps
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                                                       Indels
                          82.1%; Score 32; DB 5; Length 8; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                           AAY76794 standard; peptide; 7 AA.
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98US-00203389.
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                                                                                      1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of tumors,
                                                                                                                                                                                                                       AAY76794;
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such as cancers, autoimmune diseases, endocrine disorders, diabeticas associated complications, gastrointeetinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-aurgical pain. It may also be used for diagnosing cancer. The backbone cyclic analogues is used for imaging the existence of metastases. Somatostatin analogues can be used for the treatment patients with hormone-secreting and hormone-dependent tumours. They reduce diarrhoea through the inhibition of vasoactive intestinal peptide (VIP) secretion and by direct effect on intestinal secretion. Somatostatin analogues selective to type 2 and 5 receptors may be used for treatment of non-insulin dependent diabetes mellitus. They are useful for the prevention of atherosclerosis and restenosis. The analogues are metabolically stable, selective in their in-vivo activities and safe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                somatotropin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer; antidiaetic; antiinflammatory; somatostatin receptor ligand; atherosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis; pancreatitis; post-surgical pain.
                          group to form a cyclic structure with a moiety selected from a second building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;
or disulphide. At least one building unit is connected via a bridging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 3; Length 7;
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..... ...cerminally modified with Fmoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Backbone cyclised somatostatin analogue PTR 3181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "D form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gellerman G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP53418 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.5%;
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99WO-IL000329
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(AFAR/) AFARGAN M M.
(GELL/) GELLERMAN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7 AA;
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Modified-site
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15-JUN-1999;
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The present invention describes backbone cyclised somatostatin analogues

(I) that incorporates at least one building unit containing one nitrogen

atom of the peptide backbone connected to a bridging group (comprising an

amide, thioether, thioester or disulfield where at least one building

connected wis the bridging group to form a cyclic structure with

a moiety selected from the group consisting of a second building unit,

the side chain of an amino acid residue of the sequence or the N-terminal

connected, antidiabetic, antiarfammatory and analogust activities, and

cytostatic, antidiabetic, antiinflammatory and analogus activities, and

cytostatic, antidiabetic, autoimmune diseases, cancers, diabetic-

cytostatic, antidiabetic, autoimmune diseases, cancers, diabetic-

crastenant of atherosclerosis, autoimmune diseases, cancers, diabetic-

associated complications, endocrine disorders, inflammation,

consistent disorders, pancreatitis, post-surgical pain, and

consistent also be used in the diagnosis of cancer, by imaging

the existence of metastases, it being labeled with a detectable probe.

The present sequence represents a backbone cyclised somatostatin analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                New backbone cyclized somatostatin analogs are e.g. useful in the treatment of atherosclerosis, autoimmune diseases and cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.5%; Score 31; DB 5; Length 7; 57.1%; Pred. No. 1.7e+06; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S, Livingston BD, Grey HM;
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                                                                                                        Example 12; Page 21; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP24270 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Southwood :
Kubo RT, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-2000; 2000WO-US027766.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-354887/37.
                  WPI; 2002-681319/73.
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Matches 4; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7 AA;
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15-JUL-2002
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Baker DM,
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          The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of
                                                                                                                                                                                                                                            escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigene can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPIISOI to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.8%; Score 28; DB 4; Length 8; 50.0%; Pred. No. 1.7e+06; ive 0; Mismatches 3; Indels
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Kubo RT, Grey HM;
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(first entry)
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Matches 3; Conservative
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Celis E,
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15-JUL-2002
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ABP15891
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The present invention describes a composition (I) comprising a prepared

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group-based vaccines has several advantages over traditional vaccines, group-based vaccines has several advantages over traditional vaccines, compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of Viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (cTL and HTL), and further, to modify the immunogenicity Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. Asplication of the groups disease. Similar engineering of the response is not possible with traditional approaches. Asplication of the present in the exemplification of the present enventon. (Updated on 11-SEP-2003 to standardise OS field)
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human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (1) has virucide activity and can be used in vaccines. (1) be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines.
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Kubo RT, Grey HM;
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50.0%;
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Celis E,
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Baker DM,
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be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines group-based vaccines has several advantages over traditional vaccines compositions. There is evidence that the immune response to whole antigens in vaccine antigens is directed largely toward variable regions of the antigen, callowing for immune secape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of the sacape mutants. Furthermore, immunosupressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. Application of the present regimeering of the present repetates engences used in the examplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
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Kubo RT, Grey HM;
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particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to additional advantage of an group-based vaccine approach is the ability to combine selected groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-SEP-2003 to standardise OS field)
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group-based vaccines has several advantages over traditional vaccines,
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note= "thioether bond between A2 and A7 to form
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/note= "not a C-terminal amino acid, but condensed with
fyr(1) to form a cyclic peptide"
pharmaceutically active compounds. The present sequence represents a lanthionine bridged peptide
                                                                                                                                                                                                                                                                                   neurokinin A antagonist; tachykinin; respiratory disease; asthma; analgesic; cyclic.
                                                          Score 27; DB 6; Le.
Pred. No. 1.7e+06;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                   an N-terminal amino a
                                                                                                                                                                                                                                                                                                                                                                                                      'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                             Cyclo[-Tyr-trp-Leu-Arg-Gly-Trp-].
                                                                                                                                                                                        AAR93713 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 69; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                    "not an I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buck SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RICH ) MERRELL DOW PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US000296
                                                         h 69.2%;
Similarity 50.0%;
3; Conservative
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50.0%;
                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-336695/43.
                                                         Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                          2 YWXXXW
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                                     Sequence 8 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9521187-A1
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                                                                                                                                                                                                                                                                                                                        Synthetic
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Matches
                                                                                                                                                                   RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel lanthionine-bridged biologically active peptides e.g. vasopressin, somatostatin or enkephalin, useful as pharmaceutically active compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to lanthionine bridged peptides which are analogues of peptide compounds comprising a disulphide bridge. The disulphide bridge or thioether bond, designated a lanthionine bridge. Such analogues or lanthionine bridge peptides have improved biological activity compared to the original peptide compounds e.g. vasopressin, somatostatin, enkephalin, and endothelin. The lanthionine-bridged peptides are useful as
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                     Lanthionine bridged peptide; monosulphide bridge; thioether bond; improved biological activity; vasopressin; somatostatin; enkephalin; endothelin; pharmaceutically active compound.
                        The lanthionine bridged peptide is an analog cpd. of a naturally occurring biologically active peptide, having improved properties. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Modified by C-terminal amide (NH2) group'
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                                                                                                                     3; Indels
                                                                                             Score 27; DB 2; Length 8;
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "D-form residue. Modified by H"
                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                           ABU61730 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Page 19; 24pp; English
                                                                                                                                                                                                                                                                                               Lanthionine bridged peptide #25.
   Claim 7; Page 27; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91US-00742908.
93US-00021606.
95US-00467472.
99US-00384061.
                                                                                           69.2%;
50.0%;
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                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                     3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodman M, Osapay G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-391607/37.
                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOODMAN M.
                                                                                                                                            2 YWXXXW 7
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                                                                                                                                                                 YWKVAW
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                                                                       Sequence 8 AA;
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28-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-1999;
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                                                                                                                                                                                                                                                                         13-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                  ABU61730;
                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OSAP/)
                                                                                                                   Matches
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acid, but condensed with

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                                                                                                                                           New cyclic peptide derivs. - are neurokinin A and tachykinin antagonists useful e.g. for treating asthma or as analgesics.
                                                                                                                                                                                                                                                                                                                                The patent describes novel cyclic hexapeptide and octapeptide compounds which are antagonists of neurokinin A and which are useful medically as analgesics and for treating respiratory diseases such as asthma. The present sequence represents a specifically preferred example of the new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
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Pred. No. 1.7e+06;
0; Mismatches 3; Indels
Harbeson SL;
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The specification describes a metallo-construct, which may be a peptide, comprising metal ion-binding backbone for complexing with a metal ion and a biological function domain which is conformationally constrained upon complexing the metal ion-binding backbone with a metal ion. The peptide/metal ion complexes are less susceptible to proteolysis than the uncomplexed peptides. The peptides lack conformational restriction if not complexed to a metal ion, so that the uncomplexed peptides are either inactive or low in potency. The complexed peptides may also exhibit altered biodistribution profiles, rate of clearance from the body and bioavailability. The constructs/peptides are useful as biological, therapeutic, diagnostic imaging and radiotherapeutic agents, or in the peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metallo-constructs comprising a metal ion-binding backbone for complexing metals - and a biological function domain which may be converted from inactive to active form on binding of the construct to a metal ion.
Metallo-construct; metal ion-binding backbone; cyclic;
biological function domain; conformational restriction; radiotherapeutic;
combinatorial chemistry.

    .8
    /note= "linked with GGGC, GGC, GGGh or GGH"

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Pred. No. 1.7e+06;
0; Mismatches 2; Indels
                                                                                                                                                 'note= "D-form residue"
                                                                                                                                                                                                                          'note= "D-form residue"
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                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Somatostatin analogue peptide 3177
                                                                                                                                                                                                                                                                                /note= "ornithine"
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                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00476652.
96US-00660697.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                Misc-difference
                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                            36-JUN-1996;
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05-JUN-1996;
                                                                                                                                                                                                                                                                                                                     WO9640293-A1
                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sharma SD;
                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This peptide comprises a motif located at amino acid residues 312-319 of the galactanase of Myceliophthora thermophila CBS 117.65 (see AAW27063) and at amino acid residues 311-318 of the galactanase of Humicola insolates DR 1800 (see AAW27064). Another motif (see AAW27065) has also been identified. These motifs are characteristic of galactanases of fungi of the order Sordariales. PCR primers (see AAR35060-61) based on the motifs can be used to identify galactanase enzymes in Sordariales fungi. Such enzymes have an optimum pH above 5.8 and are useful in the food and feed industries, as well as in wine and juice processing. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                           Galactanase, fruit juice, vegetable juice, wine, pectin, depectinisation, animal feed, foodstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fungal galactanase and related DNA - useful in animal feed industry and fruit juice depectinisation.
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Pred. No. 1.7e+06;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersen LN, Clausen IG,
                                                                                                                                                                                                                                                                                                                 Corynascus heterothallicus; strain CBS 117.65.
Humicola insolens; strain DSM 1800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY02418 standard; peptide; 8 AA.
                                                                        AAW27066 standard; peptide; 8 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Somatostatin analogue peptide
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96DK-00000235
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50.0%;
                                                                                                                                                (revised)
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Best Local Similarity 50.vv,
3; Conservative
                                                                                                                                                                                                                        Galactanase peptide motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kauppinen MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVO-NORDISK AS
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01-MAR-1996;
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                                                                                                                                              17-OCT-2003
25-MAR-2003
28-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-1997.
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                                                                                                             AAW27066;
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RESULT 12
AAW27066
AAW277066
ACC AAW27
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ACC AAW27
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DT 25-MA
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Gaps ö Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic; somatotropin release inhibiting factor; somatostatin receptor subtype; synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer; antidiatabetic; antidiflammatory; somatostatin receptor ligand; atherosclerosis; autoimmune disease; diabetic-associated complication; endocrine disorder; inflammation; gastrointestinal disorder; restenosis;

/note= "D form residue"

/note= "amidated"

US2002052315-A1

02-MAY-2002

Location/Qualifiers

Misc-difference

Synthetic.

Modified-site

pancreatitis; post-surgical pain

Backbone cyclised somatostatin analogue PTR 3177.

(first entry)

19-NOV-2002

ABP53416;

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invention relates to a backbone containing an introgen at the period backbone cone building unit containing a nitrogen atom of the peptide backbone connected to a bridging group comprising an amide, thioether, thioester or disulphide. At least one building unit is connected via a bridging group to form a cyclic structure with a moiety selected from a second group to form a cyclic structure with a moiety selected from a second of building unit, side chain of or N-terminal amino acid residue. A composition containing the analogue may be used for preventing disorders such as cancers, autoimmune diseases, endocrine disorders, diabetic associated complications, gastrointestinal disorders, inflammatory diseases, pancreatitis, atherosclerosis, restenosis and post-surgical pain. It may also be used for disagnosing cancer. The backbone cyclic analogue is used for imaging the existence of metastasses. Somatostatin and hormone-dependent tumours. They reduce diarrhoea through the inhibition of vasoactive intestinal peptide (VIP) secretion and by direct
Somatostatin analogue; therapy; cyclic peptide; autoimmune disease; endocrine disorder; cancer; diabetic-associated complication; diagnosis; gastrointestinal disorder; inflammatory disease; panoreatitis; atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor; hormone-secreting tumour; hormone-dependent tumour; diarrhoea; vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclized somatostatin analogs for inhibiting growth hormone secretion from anterior pituitary and as antiproliferative agents for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  effect on intestinal secretion. Somatostatin analogues selective to type 2 and 5 receptors may be used for treatment of non-insulin dependent diabetes mellitus. They are useful for the prevention of atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a somatostatin analogue of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and restenosis. The analogues are metabolically stable, selective in
                                                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gellerman G;
                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 11; Page 61; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     their in-vivo activities and safe
                                                                                                                                                                                                                                                                         /note= "Trp-NH2"
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50.0%;
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98US-00203389
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Best Local Similarity
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                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-1998;
02-DEC-1998;
                                                                                                                                                                                                                                                                                                                  WO9965508-A1
                                                                                                                                                   Synthetic
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The present invention describes backbone cyclised somatostatin analogues

(I) that incorporates at least one building unit containing one nitrogen

atom of the peptide backbone connected to a bridging group (comprising an

amide, thioether, thioester or disulfide) where at least one building

unit is connected via the bridging group to form a cyclic structure with

a moiety selected from the group consisting of a second building unit,

the side chain of an amino acid residue of the sequence or the N-terminal

amino acid residue. (I) has antiarteriosoferotic, immunosuppressive,

cytostatic, antidiabetic, antiinflammatory and analgesic activities, and

cytostatic antidiabetic, autiinflammatory and analgesic activities, and

cytostatic antidiabetic, antiinflammatory inflammatory and analgesic activities, and

creatment of atherosclerosis, autoimmune diseases, cancers, diabetic-

associated complications, endocrine disorders, inflammation,

creatmosts. (I) can also be used in the diagnosis of cancer, by imaging

the existence of metastases, it baing labeled with a detectable probe.

The present sequence represents a backbone cyclised somatostatin analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from the present invention
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Gaps

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Score 25; DB 3; Length 7; Pred. No. 1.7e+06; Mismatches 3; Indele

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Conservative

2 YWXXXW 7

YWKVCW

ABP53416 standard; peptide; 7 AA.

ABP53416 ID ABP5 XX

New backbone cyclized somatostatin analogs are e.g. useful in the treatment of atherosclerosis, autoimmune diseases and cancers.

Gellerman G;

Hornik V, Afargan MM,

WPI; 2002-681319/73.

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(HORN/) HORNIK V. (AFAR/) AFARGAN M GELLERMAN

(GELL/)

98US-00100360. 98US-00203389. 99WO-IL000329.

19-JUN-1998; 02-DEC-1998; 15-JUN-1999;

13-DEC-2000; 2000US-00734583

Search completed: December 29, 2004, 22:23:57 Job time : 150 secs

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3; Conservative
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MOLECULE TYPE: protein
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Best Local Similarity
Matches 3; Conserv
STRANDEDNESS:
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Sequence 16, Appl
Sequence 20, Appl
Sequence 94, Appl
Sequence 53, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 17, Appli
Sequence 2, Appli
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Sequence 8, Appli
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Sequence 38, Appl
Patent No. 5185431
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                                                                       December 29, 2004, 22:13:25; Search time 37 Seconds (without alignments)
14.339 Million cell updates/sec
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.: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd.
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US-08-462-720-30

US-08-462-720-30

US-09-388-788-2

US-09-069-827A-94

US-09-069-827A-94

US-08-566-705A-17

US-09-384-061-5

US-09-384-061-5

US-09-384-061-5

US-09-125-641-1

US-09-125-641-1

US-09-125-641-1

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US-09-125-641-1

US-09-126-641-1

US-09-126-641-1

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US-09-126-641-1
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US-08-753-750B-38
5185431-15
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US-08-884-569A-14
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          GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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39
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Match Length
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                     Copyright
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Perfect score:
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100.0%; Pred. No. 3.8e+05;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-753-750B-38
Sequence 38, Application US/08753750B
Fatent No. 6610506
GENERAL IMPORMATION:
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Bother Anthony B.
APPLICANT: Pother Andrew A.
TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
US-09-430-626A-2
US-09-361-096A-46
US-09-361-096A-5
US-10-243-687-2
US-08-91-258A-5
US-08-91-258A-5
US-08-91-953A-5
US-09-91-953A-5
US-09-091-953A-5
US-09-091-953A-5
US-09-091-953A-1
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US-09-794-517A-1
US-09-794-812-1
US-09-794-812-1
US-09-794-812-1
US-09-794-812-1
US-09-794-812-1
US-09-794-812-1
US-09-794-812-1
US-09-794-812-1
US-09-636-2868-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
PRIOR APPLICATION NUMBER: GB 9324819.3
PRIOR APPLICATION NUMBER: GB 911089.7
PRILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
PRILING DATE: 03-UN-1994
INFORMATION POR SEQ ID NO: 27:
SEGURNCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 27, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEINS
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GENERAL INFORMATION:
TITLE OF INVENTION: Peptide Inhibitors of Fibronection and TITLE OF INVENTION: Related Collagen-Binding Proteins NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Lowe, Price, LeBlanc & Becker STRET: Suite 300, 99 Canal Center Plaza CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.5%; Score 24; DB 1; Length 6; 100.0%; Pred. No. 3.8e+05; ive 0; Mismatches 0; Indels
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                                                                                                                       ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
FLLING DATE: 19921110
CLASSIFCATION: 514
                                                                                             US/07/718,577
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US-07-973-235A-30
; Sequence 30, Application US/07973235A
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ATTORNEY/AGENT INPORMATION:
NAME: RODERT I. PRICE
REGISTRATION NUMBER: 22,685
REFREENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHONE: (703)684-1111
TELEFAX: (703)684-1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703)684-1124
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: Bir
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Matches 3; Conserv
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FILE REPERENCE: A34762 021645.0105
FILE REPERENCE: A34762 021645.0105
CURRENT APPLICATION NUMBER: US/08/753,750B
CURRENT FILING DATE: 1996-11-29
FRIOR FILING DATE: 1995-12-01
FRIOR PAPLICATION NUMBER: CA 2,164,274
FRIOR PILING DATE: 1995-12-01
FRIOR PILING DATE: 1995-12-01
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TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR NUMBER OF SEQUENCES: 31
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/392,841
FILING DATE: 11-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.5%; Score 24; DB 4; Length 5; 100.0%; Pred. No. 3.8e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend
ADRESSEE: Townsend and Townsend
STREET: Tower
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dower, William J.
APPLICANT: Cwirla, Steven B.
APPLICANT: Barrett, Ronald W.
TITLE OF INVENTION: PEPTIDE LIBRARY AND
TITLE OP INVENTION: SCREENING SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/07718577; Sequence 10, 5432018; Patent No. 5432018; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 3; Conserv
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;Patent No. 5185431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-753-750B-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Townsend and Townsend and Crew
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 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-069-827A-94
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                                                                                                                       RESULT 6

US-08-443-640-16

US-08-443-640-16

Sequence 16, Application US/08443640

Patent No. 5691140

GENERAL INFORMATION:
APPLICANT: NOREN, CHRISTOPHER J.
APPLICANT: BYANS, PAUL D.
TITLE OF INVENTION: WECTORS UTLIZING A SINGLE RNA POLYMERASE FOR BOTH
TITLE OF INVENTION: DIRECTIONS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS, INC
STREET: 32 TOZER ROAD
COUNTRY: US
COUNTRY: US
COUNTRY: US
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Patent No. 5849701

GENERAL INFORMATION:
APPLICANT: Roberts, David D.
APPLICANT: Sipes, John M.
APPLICANT: Sipes, John M.
APPLICANT: Negre, Mency C.
TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and TITLE OF INVENTION: Related Collagen-Binding Proteins
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%; Score 24; DB 1; Length 7; 42.9%; Pred. No. 3.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: U.S.

ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,640
FILING DATE: 18-MAY-1995
CLASSIFICATION 1945
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGESTRATION NUMBER: 30901
REFERENCY DOCKET NUMBER: NEB-102
TELECOMMUNICATION INFORMATION:
TELEFONE (508) 927-5054
TELEFONE (508) 927-1705
INPORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
TENTORY: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
Mismatches
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TYPE: amino acid
STRANDEDNESS: unknown
3; Conservative
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Matches 3, Conserv
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                                    GYWXXXW 7
                                                                       GGWSKSW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GEWRFAW 7
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US-08-462-720-30
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 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%; Score 24; DB 2; Length 7; 42.9%; Pred. No. 3.8e+05; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%; Score 24; DB 4; Length 7;
100.0%; Pred. No. 3.8e+05;
Live 0; Mismatches 0; Indels
                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-UN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT IRPORMATION:
NAME: DOW, KAREN 29,684
REGISTRATION NUMBER: 29,684
REGISTRATION NUMBER: 29,684
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 326-2420
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE (ALRAACTERISTICS:
LENGTH: 7 amino acids
                                                                        ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .Query Match
Best Local Similarity 100.0
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
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MOLECULE TYPE: peptide
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PRIOR APPLICATION NUMBER: 09/563,222 PRIOR FILING DATE: 2000-05-02 NUMBER OF SEQ ID NOS: 182 SOFTWARE: PACENTIN VEr. 2.1 SEQ ID NO 53 LENGTH: 7
                                                                                                                                                                                                                       61.5%;
                                                                                                                                                                                                                       Query Match 61.5
Best Local Similarity 100.
Matches 3; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: ENANTIOMER
LOCATION: -4
                                                                                                                                                         ; ORGANISM: Mus musculus US-09-563-222C-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMINO ACID
GY: LINEAR
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                                                                                                                                                                                                                                                                                                           1 GYW 3
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                                                                                                                                     TYPE: PRT
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Patent No. 6696620
GENERAL INFORMATION:
APPLICANT: BELCYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HIATT, ANDREW C.
CURRENT APPLICATION INWHER: US/09/563, 222C
CURRENT APPLICATION NUMBER: US/09/563, 222C
CURRENT APPLICATION NUMBER: PCT/US01/14349
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
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Sequence 94, Application US/09069827A
Patent No. 6617114
GENERAL INPORMATION:
APPLICANT: FOWLKES, Dana M
KAY, Brian K
FRELINGER, Jeffrey A
HYDE-DERVISCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
                                                                                                                                                                                                                                                                                                STATE: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,827A
FILING DATE: 31-Apr-1998
CLASSIFICATION : CURNOWN>
PRIOR APPLICATION NUMBER: US 09/050,359
FILING DATE: 31-ARR-1998
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: US 08/740,671
FILING DATE: 31-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: POWLKES=4C
TELEPHONE: (202) 73358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%; Score 24; DB 4; Length 7; 50.0%; Pred. No. 3.8e+05; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-069-827A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 94: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 50.0
Matches 3; Conservative
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US-09-563-222C-53
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Gaps
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                                                            0; Indels
Length 7;
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Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
DB 4; Le . 3.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: N/A
ANTI-SENSE: N/A
ANTI-SENSE: N/A
ANTI-SENSE: N/A
CRIGINAL TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
                            , Pred. No. 3.8
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUBAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
      Score 24;
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LOCATION: -4

LIDENTIFICATION METHOD: amino acid analysis

IDENTIFICATION METHOD: and

IDENTIFICATION METHOD: mass spectrometry

OTHER INFORMATION: water is removed and

OTHER INFORMATION: thereby

OTHER INFORMATION: a -5- bridge is present between Cys and Ser

PUBLICATION INFORMATION:

AUTHORS: JUNG, GUNTHER

AUTHORS: JUNG, GUNTHER

AUTHORS: PEPTIDES WITH SULFIDE BRIDGES AND

JOURNAL: PRECEDINGS OF THE 11TH AMERICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
ANTI-SENSE: N/A
CRIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: 1NC,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA
INMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-S
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTRRY
PAGES: 511 - 519
                                                                        COUNTRY: USA
ZIF: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAGO - IBM COMPATIBLE
OPERATING SYSTEM: MS-DGS Version 6.2
SOFTWARE: ASCIT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FLING DATE: 6-JUNE-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REGISTRATION NUMBER: 27,224
REGISTRATION INFORMATION:
TELEFRAM: (212) 697-3355
TELEFRAM: (212) 697-3355
TELEFRAM: (212) 557-5635
TELERAM: NONE
SEQUENCE CHARACTERISTICS:
LENGTH: 8
LENGTH: 8
LENGTH: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: ENANTIOMER LOCATION: -4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINO ACID
GY: LINEAR
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                        NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SILLEDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%; Score 24; DB 3; Length 8; 33.3%; Pred. No. 3.8e+05; Live 1; Mismatches 3; Indels
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Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                    PAGES: 865 - 869
DATE: 1990
DOCTURENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHICNINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - FIRE
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STRUCTURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: 0
PUBLICATION INFORMATION:
AUTHORS: BEAN, WARK F.
TITLE: IDENTIFICATION OF A THIOSTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELEVANT RESIDUES IN SEQ ID NO: RELEVANT RESIDUES IN SEQ ID NO: US-08-467-472C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
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Best Local Similarity 33.3
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATE: 1986
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PUBLICATION DATE
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3 FWKTSW 8
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JOURNAL:
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US-08-467-472C-6
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JOCATION: 1..2
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "Phe is in the D conformation and is
OTHER INFORMATION: linked to DTPA;
NAME/KEY: Modified-site
LOCATION: 1..4
OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
OTHER INFORMATION: is L-chlorophenylalanine; the Trp is in the
PERTURE:
NAME/KEY: Modified-site
LOCATION: 7..8
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /label= Variant residues
OTHER INFORMATION: /note= "The carboxyl group of the C-terminal
OTHER INFORMATION: /note= "The carboxyl group of the C-terminal
US-08-586-670A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODWAN, WURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERNCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
Modified-site
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DESCRIPTION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10016
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
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NAME/KEY:
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                 PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.

TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%; Score 24; DB 3; Length 8; 33.3%; Pred. No. 3.8e+05; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-586-670A-17

Sequence 17, Application US/08586670A

Sequence 17, Application US/08586670A

PAPLICANT: MCBride, William

APPLICANT: MCBride, William

APPLICANT: Dean, Richard T.

TITLE OF INVENTION: Somatostatin Derivatives

TITLE OF INVENTION: And their Radiolabeled Products

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSES: Banner & Witcoff, Ltd.

STREET: IO South Wacker Drive, Suite 3000

CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 60606

ZIP: 60606

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/586,670A

FLING DATE: 22-APR-1996

CLASSIFICATION: 424

ATORNEY/AGENT INFORMATION:

NAME: NO. 6241965nan, Kevin E

REGISTRATION NUMBER: 35,303

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 35,303

RELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   DATE: 1990
DOCUMENT NUMBER:
PILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
                                                                                                                                                                                                             PROCEEDINGS OF THE 11TH AMERICAN
                                                                                                                                                                                                                                                           JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
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Best Local Similarity
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                               443 - 445
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JOURNAL:
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PAGES:
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FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
HUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
ITTLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY-PRODUCT
IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
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ANTI-SENSE: N/A
PRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES:
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDINGS IN SEQ ID NO: 5: CYS-SER PUBLICATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNE: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5: CYS-SER
STRUCTURE
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PROCEEDINGS OF THE 11TH AMERICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOBETHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOCUMENT NUMBER:
FILLING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5:
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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
RELEVANT RESIDUES IN SEQ ID NO:
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ESCOM (LEIDEN 1990)
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Best Local Similarity 33.3
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
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JOURNAL:
JOURNAL:
VOLUME: E
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LOCATION: -4

IDENTIFICATION METHOD: amino acid analysis

IDENTIFICATION METHOD: and

IDENTIFICATION METHOD: and

IDENTIFICATION METHOD: anse spectrometry

OTHER INFORMATION: water is removed and

OTHER INFORMATION: thereby

OTHER INFORMATION: a -S - bridge is present between Cys and Ser

PUBLICATION INFORMATION:

AUTHORS: JUNG, GUNTHER

TITLE: PEPTIDES WITH SILLEIDE BRIDGES AND

JOURNAL: PEPTIDES

JOURNAL: SYMPOSIUM

VOLUME: ESCOM (LEIDEN 1990)
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ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: ANINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: 1NC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
Sequence 6, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GCODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
                                                                                                                                                                                                                                                                        ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPA - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII DATA:
APPLICATION NUMBER: US/09/384,061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILLING DATE:
PILLING DATE:
APPLICATION NUMBER: US 08/021,606
PILLING DATE: 28-JANUARY-1993
ATTORNEY AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGIETRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LAR-9122B
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 697-3355
TELEFAX: (212) 557-5635
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 557-56:
TELEX: NONE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
DESCRIPTION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: ENANTIOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             865 - 869
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                                                                                                                                                                                                       NEW YORK
                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                               CITY: NEW
STATE: NY
COUNTRY:
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Gaps ;;

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RESULT 15

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RELEVANT RESIDUES IN SEC. IN SEC. IN PUBLICATION INFORMATION:

AUTHORS: SHIBA, TETSUO

TITLE: CHEMISTRY OF LAWTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUNE: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE: PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAM, MARK F.
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY-PRODUCT
TITLE: BY-PRODUCT
TITLE: BY-ROCEDINGS OF THE 11TH AMERICAN
JOURNAL: PREPTIDE
JOURNAL: PREPTIDE
JOURNAL: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
PUBLICATION DATE:
PUBLICATION DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-6
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Search completed: December 29, 2004, 22:27:50 Job time : 38 secs

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82.1%; Score 32; DB 13; 1
100.0%; Pred. No. 1.5e+06;
ive 0; Mismatches 0;
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US-10-046-922-68
; Sequence 68, Application US/10046922
                                          7; Conservative
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Best Local Similarity
Matches 7; Conserv
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 TYPE: PRT
ORGANISM: peptide
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Sequence 586, Appl
Sequence 525, Appl
Sequence 496, Appl
Sequence 496, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 38, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
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                                                                                               December 29, 2004, 22:27:17 ; Search time 140 Seconds (without alignments) 20.556 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: \( \cgn2_6 \) \text{prodata} 2 \) \text{Pubpaa} \( \text{VSOT} \) \text{PUBCOMB.pep:*} 2: \( \cgn2_6 \) \text{prodata} 2 \) \text{Pubpaa} \( \text{VSOT} \) \text{PUBCOMB.pep:*} 3: \( \cgn2_6 \) \text{prodata} 2 \) \text{Pubpaa} \( \text{VSOT} \) \text{PUBCOMB.pep:*} 4: \( \cgn2_6 \) \text{prodata} 2 \) \text{Pubpaa} \( \text{VSOT} \) \text{PUBCOMB.pep:*} 5: \( \cgn2_6 \) \text{prodata} 2 \) \text{Pubpaa} \( \text{VSOT} \) \text{PUBCOMB.pep:*} 7: \( \cgn2_6 \) \text{prodata} 2 \) \text{Pubpaa} \( \text{VSOT} \) \text{PUBCOMB.pep:*} 7: \( \cgn2_6 \) \text{prodata} 2 \) \text{Pubpaa} \( \text{VSOT} \) \text{PUBCOMB.pep:*} 9: \( \cgn2_6 \) \text{prodata} 2 \) \text{Pubpaa} \( \text{VSOT} \) \text{PUBCOMB.pep:*} 9: \( \cgn2_6 \) \text{prodata} 2 \) \text{Pubpaa} \( \text{VSOT} \) \text{PUBCOMB.pep:*} 10: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 12: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 13: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 13: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 15: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 16: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 17: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 18: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 18: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 18: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 18: \( \cgn2_6 \) \text{prodata} 2 \( \text{Pubpaa} \) \text{VSOT} \( \text{PUBCOMB.pep:*} \) 18: \( \cgn2_6 \) \text{Prodata} 2 \( \text{Pubpaa} \) \( \text{VSOT} \) \( \text{PUBCOMB.pep:*} \) 18: \( \cgn2_6 \) \( \text{PUBCOMB.pep:*} \) 18: \( \cgn2_6 \) \( \text{P
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              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-046-922-68
US-10-190-082-58
US-10-436-549-496
US-10-436-549-525
US-10-712-425-525
US-10-712-425-525
US-10-718-943-48
US-10-346-737A-45
US-09-563-222-53
US-09-563-222-53
US-10-475-853-67
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Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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Sequence 133, App
Sequence 267, equence 13, App
Sequence 13, App
Sequence 14, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 65, Appl
           Sequence 5, Appli
Sequence 179, App
Sequence 180, App
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Sequence 12, Appli
Sequence 6, Appli
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Sequence 1, Appl
                                                  Sequence 179, A
Sequence 180, A
Sequence 279, A
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Koivunen, Erkki
APPLICANT: Koivunen, Erkki
APPLICANT: Kubo, Hajime
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 2896/7370848.
CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 67
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (4)..(6)
OTHER INFORMATION: X at position 4-6 is any amino acid
US-10-046-922-67
       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 67, Application US/10046922
Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alltalo, Kari
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Gape

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Length 7; 0; Indels

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PAPPLICANT: Zhang, snenganesus,
APPLICANT: Zhang, snenganesus,
APPLICANT: Bankovic, Scephen J.
TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
TITLE OF INVENTION: PROTOEN ANALYSIS
FILE REPERENCE: ENGS-PO1-001
CURRENT FILING DATE: 2002-05-12
FRICH PRILOR DATE: 2002-05-10
FRICH APPLICATION NUMBER: 60/393,233
FRICH FILING DATE: 2002-07-01
FRICH PRILOR DATE: 2002-07-01
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| Sequence 525, Application US/10436549
| Publication No. US20040038307A1
| GENERAL INFORMATION:
| APPLICANT: Lee, Frank D.
| APPLICANT: Lee, Frank D.
| APPLICANT: Chan, John W.
| APPLICANT: Chan, John W.
| APPLICANT: Chan, John W.
| APPLICANT: Chan, John W.
| APPLICANT: Chan, John W.
| APPLICANT: Chan, John W.
| APPLICANT: Chan, John W.
| APPLICANT: Chan, John W.
| APPLICANT: Chan, John W.
| APPLICANT: Chan, John W.
| TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
| TITLE OF INVENTION: UNIQUE RECOGNITION NUMBER: 60/339, 626
| PRIOR APPLICATION NUMBER: 60/339, 235
| PRIOR PLING DATE: 2002-07-01
| PRIOR PLING DATE: 2002-07-01
| PRIOR PLING DATE: 2002-07-01
| PRIOR PLING DATE: 2002-07-01
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PRIOR APPLICATION NUMBER: 60/393,223
PRIOR FILING DATE: 2002-07-01
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Best Local Similarity
Matches 3; Conserv
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Publication No. US20020164667A1
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Koivunen, Erkki
APPLICANT: Kulovunen, Erkki
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
FILE REFERENCE: 28967/37084A
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Pred. No. 1.5e+06;
0; Mismatches 3; Indels
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| Sequence 586, Application US/10190082
| Publication No. US20030148264A1
| GENERAL INFORMATION:
| APPLICANT: Lasky, Lawrence A. |
| APPLICANT: Held, Heike A. |
| TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS |
| TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS |
| CURRENT APPLICANTON NUMBER: US/10/190,082 |
| CURRENT PPLICATION NUMBER: US 60/303,634 |
| PRIOR PPLICATION NUMBER: US 60/303,634 |
| NUMBER OF SEQ ID NOS: 683 |
| SEQ ID NO 586 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.1%; Score 32; DB 13; I
100.0%; Pred. No. 1.5e+06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/046,922
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.0
SEQ ID NO 68
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
LOCATION: (4)..(6)
OTHER INFORMATION: X is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (8)...(8)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-68
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Publication No. US20040038307A1
GENERAL INFORMATION:
APPLICANT: Hee, Frank D.:
APPLICANT: Meng, Dr. Xun
APPLICANT: Chan, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.v
and 3; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-436-549-496
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GENERAL INFORMATION:
APPLICANT: LEE, FRANK D.
APPLICANT: LEE, FRANK D.
APPLICANT: LEE, FRANK D.
APPLICANT: LIVINGSTON, DAVID
ITILE OF INVENTION: PROTECME EDITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN
TITLE OF INVENTION: MODIFICATION ANALYSIS
FILE REFERENCE: ENGE-PO2-05-10
FILE REFERENCE: ENGE-PO2-05-10
FRIOR APPLICATION NUMBER: 60/393,137
PRIOR APPLICATION NUMBER: 60/393,137
PRIOR APPLICATION NUMBER: 60/393,137
PRIOR PILING DATE: 2002-07-01
PRIOR PILING DATE: 2002-07-01
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; Sequence 48, Application US/10418943
; Publication No. US20040002441A1
; GENERAL INFORMATION:
; APPLICANT: Segall, Anca
; APPLICANT: Pinilla, Clemencia
; TITLE OF INVENTION: FRCOMBINATION MODULATORS AND METHODS
; TITLE OF INVENTION: FOR PRODUCING AND USING THE SAME
; FILE REFERENCE: 011443 008-999
; CURRENT APPLICATION NUMBER: US/10/418,943
; CURRENT FILING DATE: 2003-04-17
; PRIOR FILING DATE: 2000-06-22
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Pred. No. 1.5e+06;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 6
                                                                                                                  Sequence 525, Application US/10712425 Publication No. US20040180380A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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CORGANISM: Homo sapiens
US-10-712-425-525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                    Publication No. US2 GENERAL INFORMATION
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Fublication No. US20040180380A1
GENERAL INCORMATION:
APPLICANT: LEE, FRANK D.
APPLICANT: LEE, FRANK D.
APPLICANT: LEE, FRANK D.
APPLICANT: LEE, FRANK D.
APPLICANT: LEE, FRANK D.
APPLICANT: LEE, FRANK D.
APPLICANT: LEE, FRANK D.
APPLICANT: LIVINGSTON, DAVID
TITLE OF INVENTION: MODIFICATION ANALYSIS
TITLE OF INVENTION: MODIFICATION ANALYSIS
CURRENT APPLICATION NUMBER: 60/379,66
FRIOR PILING DATE: 2002-07-01
FRIOR PILING DATE: 2002-07-01
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 1.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/430,948
PRIOR FILING DATE: 2002-12-04
PRIOR PILING DATE: 2002-12-04
PRIOR FILING DATE: 2002-12-13
PRIOR PELING DATE: 2002-12-13
PRIOR PELING DATE: 2002-12-13
PRIOR PELING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 614
SOFTWARE: PATENTIN VETRION 3.2
SEQ ID NO 525
LENGTH: 5
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 100
Matches 3; Conservative
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CORGANISM: Homo sapiens
US-10-712-425-496
                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Human
US-10-436-549-525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GYW 3
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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-53
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; ORGANISM: Homo sapiens
US-10-403-938-27
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                      JS-09-563-222-53
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US-10-475-853-6
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Sequence 45, Application US/10346737A

Publication 0. US20040142379A1

Sequence 45, Application US/10346737A

Publication No. US20040142379A1

GENERAL INFORMATION:

APPLICANT: St. Hilaire, Phaedria

TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS

TITLE OF INVENTION NUMBER: US/10/346,737A

CURRENT PILING DATE: 2003-01-16

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.1

SEQ ID NO 45

LENGTH: 6
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Sequence 38, Application US/09884767A

Publication No. US2020192789A1

GENERAL INFORMATION:

APPLICANT: Low, Arthur C.

APPLICANT: Loueau, Christopher J.

APPLICANT: Ladner, Robert C

TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES

FILE REPREMENT: DXX-012.1 US, DXX-012.1 PCT

CURRENT APPLICATION NUMBER: US, 09/597,321

PRIOR APPLICATION NUMBER: US 09/597,321

PRIOR PILING DATE: 2001-06-19

NUMBER OF SEQ ID NOS: 217

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 217

LENGTH. 3
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US-09-884-767A-38
                  61.5%; Score 24; DB 15; Length 6; 50.0%; Pred. No. 1.5e+06; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.5%; Score 24; DB 16; Length 6; 100.0%; Pred. No. 1.5e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.5%; Score 24; DB 9; Length 7; Best Local Similarity 100.0%; Pred. No. 1.5e+06; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 3; Conservative
                                                                                                     2 YWXXXW 7
                                                                                                                                      1 YWCYWW 6
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Publication US/10475853
Publication No. US20040121442A1
Publication No. US20040121442A1
Publication No. US20040121442A1
REDREAL INFORMATION:
APPLICANT: Chet, Ilan
APPLICANT: Viterbo, Ada
TITLE OF INVENTION: PROMOTERS OF SAME AND USES THEREOF
FILE REFERENCE: 27049
CURRENT APPLICATION NUMBER: US/10/475,853
CURRENT APPLICATION NUMBER: US/10/475,853
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/10403938

Publication No. US20040025195A1

Publication No. US20040025195A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
TITLE OF INVENTION: NOVEL:
TITLE OF INVENTION: NOVEL:
TITLE OF INVENTION NUMBER: US/10/403,938

CURRENT FILING DATE: 2003-03-28

NUMBER OF SEQ ID NOS: 88

SOFTWARE: PARCENT NOVE: 88

SOFTWARE: PARCENT NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOVEL: NOV
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Sequence 53, Application US/09563222
Publication No. US20030079253A1
GENERAL INFORMATION:
APPLICANT: Heart, Andrew
TITLE OF INVENTION: IMMUNOSLOBULIN BINDING PROTEIN ARRAYS IN
TITLE OF INVENTION: EURANYOTIC CELLS
FILE REPERENCE: 310.098.406
CURRENT FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PASTERO for Windows Version 4.0
SOFTWARE: PASTERO for Windows Version 4.0
SOFTWARE: PASTERO for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
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US-09-852-870A-5
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US-10-783-950-53

is Sequence 53, Application US/10783950

is Dequence 53, Application No. US20040199945A1

is GENERAL INFORMATION:

APPLICANT: EPICYTE PHARMACEUTICALS, INC.

APPLICANT: HIATT, ANDREW C.

APPLICANT: HIATT, ANDREW C.

TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS

FILE REFERENCE: 068904-0501

CURRENT APPLICATION NUMBER: US/10/783,950

CURRENT FILING DATE: 2004-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

SEQ ID NOS: 182

SEQ ID NO 53

LENGTH: 7

LENGTH: 7

LENGTH: 7

LENGTH: 7

LENGTH: 7
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Sequence 5, Application US/09852870A

Patent No. US2002016513A1

GENERAL INFORMATION:
APPLICANT: Goodman, Murray
APPLICANT: Goodman, Murray
FILE REFERENCE: LKR 9122-D

CURRENT APPLICATION NUMBER: US/09/852,870A

FILE REPERENCE: LKR 9122-D

CURRENT FILING DATE: 2001-05-10

PRIOR FILING DATE: 1999-08-26

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin version 3.0

LENGTH: 8
                                                                                                                                                                    Query Match
61.5%; Score 24; DB 16; L
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
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61.5%; Score 24; DB 17; L
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
                     iENGTH: 7
CYPE: PRT
COGANISM: Artificial sequence
FRATURE:
FRATURE:
JOHER INFORMATION: peptide derived from chit36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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CORGANISM: Mus musculus
US-10-783-950-53
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1 GYW 3
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US-09-852-870A-5
SEQ ID NO 6
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B31263 PT0519 PT0641 PT0726 PT0726 PT1946 PD0028 AD10028 I79564 S09652 PP0727 PP1602 PT0526 PT0526

ALIGNMENTS

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5.1.6
Compugen Ltd
version :
- 2004 (
GenCore (c) 1993
        Copyright
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using sw model - protein search, OM protein

December 29, Run on:

2004, 22:13:51 ; Search time 38 Seconds (without alignments) 20.256 Million cell updates/sec

US-10-046-922-68 39 1 GYWXXXWX 8 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

909 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 8 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
3: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

gut pentapeptide T-cell receptor be
cerebellar degener
T-cell receptor be
dermorphin (Trp-4,
T-cell receptor be
tubulin beta-3 cha
globulin ly alpha
ameletin - rat
dermorphin - Rohde fatty-acid synthas glutathione transf dermorphin (Lys-7) IG H chain V-D-J r leucokinin V - Mad bradykinin-potenti RPCH-related neuro T-cell receptor be C-cell receptor be cholecystokinin-5 Description Query Match Length Result Š

T-cell receptor be T-cell receptor be bradykinin-potenti

neuropeptide - sea Ig heavy chain CRD Ig heavy chain CRD

B53284 PT0661 A32516 A60803 PT0281 PT0308 PT0729 PT0580

alcohol dehydrogen dnaA protein - Pse dihydrofolate redu

RESULT 1 JH0253 gtt pentapeptide - Japanese eel C;Species: Anguilla japonica (Japanese eel) C;Species: Anguilla japonica (Japanese eel) C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995 C;Accession: JH0253 R;Useaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M. B;Ochem. Biophye. Res. Commun. 180, 828-832, 1991 A;Title: Structure and function of a pentapeptide isolated from the gut of the eel. A;Reference number: JH0253; MUID:92062113; PMID:1953755 A;Accession: JH0253 A;Molecule type: protein A;Residues: 1-5 <ues> A;Experimental source: gut C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastr; and of the circular muscle of the gastro-intestinal junction.</ues>
Query Match Best Local Similarity 66.7%; Pred. No. 2.88+05; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYW 3   1:  Db 1 GFW 3
RESULT 2 PT0532 T-cell receptor beta chain V-D-J region (100-4AJ) - mouse (fragment) T-cell receptor beta chain V-D-J region (100-4AJ) - mouse (fragment) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
Kireney, A. Med. 174, 115-124, 1991 J. Exp. Med. 174, 115-124, 1991 A,Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A,Reference number: PT0509; MUID:91277601; PMID:1711558 A,Accession: PT0532
A;Status: translation not shown A;Molecule type: mRNA A;espesidues: 1-6 <fee. A;Experimental source: adult thymus, strain BALB/c C;Keywords: T-cell receptor</fee. 
Query Match Best Local Similarity 66.7%; Pred. No. 2.88+05; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 GYW 3         Db 4 GNW 6

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R.Hinz, U.; Wolk, A.; Renkawitz-Pohl, R. Development 116, 543-554, 1992
A.Fitle: Ultrabithorax is a regulator of beta-3 tubulin expression in the Drosophila visc A.Reference number: S33567; WUID:93170162; PMID:1363225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT:P08841; EMBL:X68393; NID:g7669; PIDN:CAA48459.1; PID:g4377448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
N;Alternate names: 11S globulin alpha subunit gamma chain
N;Alternate names: 11S globulin alpha subunit gamma chain
C;Species: Cucurbita sp. (cucurbit)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
C;Accession: S09478
R;Ohmiya, M.; Hara, I: Matsubara, H.
Plant Cell Physiol. 21, 157-167, 1980
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and A;Reference number: S09066
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: PT0728
R;Remery, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Status: translation not shown
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                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S33567
       Gaps
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    mouse (fragment)

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A,Residues: 1-7 «FEBS
A,Experimental source: newborn thymus, strain BALB/c
C,Reywords: T-cell receptor
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Pred. No. 2.8e+05;
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50.0%; Pred. No. 2.8e+05;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     T-cell receptor beta chain V-D-J region (161-2H)
       Mismatches
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A;Introns: 5/3
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                         Sassance degeneration-related protein - mouse (fragment)
Carebellar degeneration-related protein - mouse (fragment)
Cassecies; Mus musculus (house mouse)
Caste: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
Cacession: B35640
Raccension: B35640
Aaritle: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal max Aareference number: A35640; MUID:90222173; PMID:2326268
Aaritle: Cerebellar degeneration-related antigen: Aimit and Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference number: Aareference num
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dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
c;Species Phyllomedusa bicolor (two-colored leaf frog)
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C;Accession: S21230
C;Accession: S21230
C; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G. FBS Lett. 302, 151-154, 1992
A;Title: Identification and characterization of two dermorphins from skin extracts of the A;Reference number: S21152; MUID:92339502; PMID:1633846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0629
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH
A;Accession: PT0528
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A;Molecule type: protein
A;Residues: 1-7 <MIG>
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
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C;Species: Mus musculus (house mouse)
C;bacies: J-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
R;Feeney, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.9%; Score 14; DB 2; Length 6; 50.0%; Pred. No. 2.8e+05;
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A;Molecule type: mRNA
A;Residues: 1-6 <FE2>
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Best Local Similarity 66.7
Matches 2; Conservative
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C;Accession: A60139
R;Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
Biochim. Biophys. Acta 828, 380-382, 1985
Biochim. Biophys. Acta 828, 380-382, 1985
Biochim. Biophys. Acta 828, 380-382, 1985
Birtle: Amino acid sequence around the reactive serine residue of the thioesterase doma;
A;Title: Amino acid sequence around the reactive serine residue of the thioesterase doma;
A;Reference number: A60139; MUID:85175165; PMID:3921056
BiRcession: A60139
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NyAlternate names: glutathione S-transferase class mu 9
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Ciscession: S71870
Ricession: S71870
Biochem. J. 317, 879-884, 1996
A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray
A;Reference number: S71876
A;Accession: S71870
A;Accession: S71870
A;Accession: S71870
A;Accession: S71870
A;Accession: S71870
C;Comment: At least five species-independent classes of cytosolic glutathion transferases
C;Comment: At least five species-independent classes of cytosolic glutathion transferases
C;Complex: dimer
C;Complex: dimer
C;Complex: dimer
C;Complex: detering a nucleophilic conjugation of intracellular glutathione to a valuethway: detoxification; xenobiotics metabolism
A;Description: catalyzes the nucleophilic conjugates facilitates their further metabolism
A;Description: catalyzes
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C;Species: Phyllomedusa bicolor (two-colored leaf frog)
C;Species: D-bcc-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
C;Accession: S36662
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.;
FRBS Lett. 302, 151-154, 1992
A;Fitle: Identification and characterization of two dermorphins from skin extracts of the
A;Reference number: S21152; MUID:92339502; PMID:1633846
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A;Molecule type: protein
A;Residues: 1-7 <MIG>
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R;Montecucchi, P.C.; De Castiglione, R.; Brspamer, V.
Int. Dett. Protein Res. 17, 316-321, 1981
A,Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz A,Reference number: A61324; MUID:82029915; PMID:7287302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: A61411
R;Burzynaki, S.R.
Anal: Blochem. 70, 359-365, 1976
A;Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the
A;Reference number: A61411; MUID:76182447; PMID:1267130
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A;Molecule type: protein
A;Residues: 1-7 <MON-
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology
C;Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin
F;Z/Modified site: D-alanine (Ala) #status experimental
F;Z/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;Z/Modified site: amidated carboxyl end (Ser) #status experimental
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fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Sep_1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
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|Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
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                                                                                                                                                                     Length 4;
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status
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100.0%; Pred. No. 2.8e+05;
:ive 0; Mismatches 0;
                                                                                                                                                             33.3%; Score 13; DB 100.0%; Pred. No. 2.6 tive 0; Mismatches
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    A;Accession: S09478
A;Molecule type: protein
A;Residues: 1-4 <OHM>
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Residues: 1-6 <BUR>
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RESULT 14
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Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
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C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0315
A;Aither is locken. Physiol. C 88, 27-30, 1987
A;Aither is solation, primary structure, and synthesis of leucokinins V and VI: myotropic
A;Reference number: JS0315
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            33.3%; Score 13; DB 2; Length 7; 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0; Indels
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ative 0; Mismatches 0;
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A;Residues: 1-8 «LEV»
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin
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leucokinin V - Madeira cockroach
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Search completed: December 29, 2004, 22:28:34 Job time : 39 secs

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Q9bry4 homo sapien
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G61dps pseudomonas
Q9r5r2 shigella dy
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version 5.1.6
- 2004 Compugen Ltd.
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TYPY PACDA
TYSI LITRU
WWA1 ACHFU
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
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Perfect score:
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borrelia bu
borrelia bu
enterobacte
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conus purpu
periplaneta
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gryllus bim
                                          human immun
                                                                                libellula a
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tabanus atr
                                                                                              melolontha
                                                                                                                                      cyphononyx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDINDE-1853788; MEDINDE-95156893; PubMed=7853788; MEDINDE-95156893; PubMed=7853788; Makazato H., Hattori S., Ushijima T., Matsuda T., Yoshioka K., Endo F., Matsuda I.; "Mutations in the COL4A5 gene in Alport syndrome: a possible mutation
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Fisher;
STRAIN=Fisher;
STRAIN=95331633; PubMed=7607556;
Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
Henderson T., Owens G.A., Danner D.B., Jupe B.R., Dell'Orco R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McClung J.K.;
"Regions of evolutionary conservation between the rat and human prohibitin-encoding genes.";
Gene 158:291-294 (1995).
EMBL; U17178; AAA86692.1; --
NON TER
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              Q8g104
Q8kms9
Q8kms9
Q8de81
P14086
P25418
P25423
P61856
P14595
P14595
P30369
P30369
P30369
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Pred. No. 1.8e+06;
0; Mismatches 3; Indels
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                      8 AA.
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                                       ÖBUEBI
AKHI GRYBI
AKHI LIBAU
AKHI MELML
AKHI PROTE
AKHI TABAT
C125 CYPDO
CCKN MACEU
COKN MACEU
COKN MACEU
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02-WAR-2004 (TrEMBLrel. 27, Last sequ
WARR-2004 (TrEMBLrel. 27, Last anno
Collagen alpha 5(IV) chain (Fragment)
                                                                                                                                                                                                                                                                                                                 Created)
              Q8GL04
Q8KMS9
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G62721 062721
01-NOV-1996 (TERMELRE1 01, L.
01-NOV-1996 (TERMELRE1 01, L.
01-NOV-1998 (TERMELRE1 06, L.
Problibitin (Pragment)
Rattus norvegicus (Rat).
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nes 2; Conservative
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2; Conservative
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P58649;
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OCP3_OCTM1
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-- MISCELLANGOUS: On the 2D-gel the determined pl of this unknown protein is: 6.6, its MW is: 19 kDa.
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                                                                                            Gaps
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MEDLINE-2238825; PubMed=12477932;
RIABBEAGE R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jorden H., Moore T., Max S.I., Wang J., Hsieh F.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                     01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
Mus musculus (Mouse).
                                                                   51.3%; Score 20; DB 2; Length 8; 40.0%; Pred. No. 1.8e+06; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AA; 717 MW; 7364087043100000 CRC64;
                                             8 AA; 933 MW; 7370437735BAB378 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AA.
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in primordial germ cells.";
Kidney Int. 46:1307-1314(1994).
EMBL; S75903; AABB3374.1; -.
NON TER 1 1
SEQÜENCE 8 AA; 933 MW; 7370º
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BRY4;
01-JUN-2001 (TrEMBLrel. 17,
                                                                                Local Similarity 40.0
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Matches 2; Conservative
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                                                                                                                 3 WXXXW 7
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P38639;
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SEQUENCE
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UF01 MOUSE
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Q9BRY4
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GO; GO:0019901; F:Strdemain kinase binding; ISS.
GO; GO:0042169; F:Strdemain binding; ISS.
GO; GO:0043130; F:Strdemain binding; ISS.
GO; GO:0043130; F:Uniquitin binding; ISS.
GO; GO:004314; P:Unitracellular signaling cascade; ISS.
GO; GO:0045944; P:positive regulation of transcription from P. ..; ISS.
GO; GO:0008104; P:progulation of I:kappaB kinase/NF-kappaB cas. ..; ISS.
GO; GO:0006950; P:response to stress; ISS.
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Wuzuy D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchwan J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iwakoshi E., Hisada M., Minakata H.;
"Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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-- FUNCTION: Cardioactive, has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Octopodiformes, Octopoda, Incirrata, Octopodidae, Octopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.0%; Score 16; DB 2; Length 7; 66.7%; Pred. No. 1.8e+06; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC005857; AAH05857,3; _...
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               779 MW; 737728769DDDD6F0 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-UIL-2004 (Rel. 44, Last annotation update)
05-UIL-2004 (Rel. 46, Last annotation occupate)
0ctopus minor (Octopus).
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-!- PTM: Ocp-4 has D-Ser instead of L-Ser.
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PROSITE; PS01357; ZF ZZ 1; UNKNOWN 1.
PROSITE; PS0135; ZF ZZ 2; 1.
SEQUENCE 7 AA; 779 MW; 737728769DI
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InterPro; IPR000433; Znf_ZZ.
Pfam; PF00569; Zz].
SMART; SM00165; UBA; 1.
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Best Local Similarity
Matches 2; Conserv
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01-DEC-2001 (Tr)
Df (Fragment).
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01-JUL-1997
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01-FEB-1997
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-I- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1. D-amino acid; Direct protein sequencing; Hormone.

2 2 2 2 2 2 SEQÜENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;
                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequences at the 5'-termini of the alfalfa mosaic virus RNAs and the intercistronic junction in RNA 3."; Nucleic Acids Res. 8:5635-5647(1980).
EMBL; V00047; CAA23416.1; -
1 1.1.
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Alfalfa mosaic virus.
Alfalfa mosicive-strand viruses, no DNA stage; Bromoviridae;
Alfamovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=81124289; PubMed=6927843;
Koper-Zwarthoff B.C., Brederode P.T.M., Veeneman G., van Boom J.H.,
Bol J.F.;
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"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-I. SIMILARITY: Belongs to the allatostatin family.
Amidation; Direct protein sequencing; Neuropeptide.
MOD RES
8 Leucine amide.
SEQÜENCE 8 AA; 898 MW; 922879CABB58640D CRC64;
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Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Buksayota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.

NCBI_TaxID=82600;
                                                                                                     Score 15; DB 1; Length 4; Pred. No. 1.8e+06; 0; Mismatches 1; Indels
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Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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MEDLINE=98054539; PubMed=9392829;
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Similarity 66.7%;
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"Evidence for insufficient chondrocytic differentiation during repair of full-thickness defects of articular cartilage.";
Matrix Biol. 15:39-47(1996).
EMBL; S83371; AAD14433.1; -.
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MEDLINE-97315886; PubMed-9171891;
MEDLINE-97315886; PubMed-9171891;
Chen H.T., Alexander C.B., Chen F.F., Mage R.G.;
"Rabbit DQ52 and DH gene expression in early B-cell development.";
MO1. Immunol. 33:1313-1321(1996).

EMBL; U62585; AAB18735:1; -.
                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pro alpha 1 type III collagen protein (Fragment).
Name-pro alpha 1 type III collagen;
Orytcolagus cuniculus (Rabbit).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
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SEQUENCE FROM N.A.
MEDLINE=90202723; PubMed=2156808;
Pritchard A.E., Vasil M.L.;
Prossible insertion sequences in a mosaic genome organization upstream of the exotoxin A gene in Pseudomonas aeruginosa.";
J. Bacteriol. 1772:202-2028(1990).
EMBL; M27186; AAA26012.1;
EMBL; M27175; AAA26011.1;
...
                                                                                                                                                                                                                                                                                          (strain Ps188) toxA gene encoding exotoxin A, S' end ((strain PA103) toxA gene encoding exotoxin A, S' end) (Fragment).
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Enterobacteriaceae, Shigella.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Polard P., Prere M.F., Chandler M., Fayet O.;
"Programmed translational frameshifting and initiation at an in gene expression of bacterial insertion sequence IS911.";
J. Mol. Biol. 222:465-477(1991).
NON TER
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   DB 2; Length 8;
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33.3%; Score 13; DB 2; L6
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.
NCBI_TaxID=204181;
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Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
"Phylogeny and evolution of basils and allies (Ocimeae, Labiatae) based on three plastid DNA regions.";
Mol. Phylogenet. Evol. 31:277-299(2004).
EMBL, AJ505379; CAD45500.1; -.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
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Ribosomal protein (Fragment).
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Lamiaceae; Nepetoldeae; Ocimeae; Plectranthus.
NCBI_TaxID=204181;
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Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
"Phylogeny and evolution of basells and allies (Ocimeae, Labiatae)
based on three plastid DNA regions.";
Mol. Phylogenet. Evol. 31:277-299(2004).
EMBL, AJSO5427; CAD45547.1; -.
Chloroplast; Ribosomal protein.
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"Phylogeny and evolution of basils and allies (Ocimeae, Labiatae) based on three plastid DNA regions.";
Mol. Phylogenet. Evol. 31:277-299(2004).
EMBL; AJ505379; CAD45500.1; -.
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lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
NCBI_TaxID=204226;
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Ribosomal protein (Fragment).
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DE Ribosomal
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Compugen Ltd.
version:
GenCore
Copyright (c) 1993
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	December 30, 2004, 12:55:07; Search time 55.6981 Seconds
using sw model	2004, 12:55:07
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OM protein -	Run on:

		(without alignments) 51.525 Million cell update
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Title:	US-10-046-922-68	
Perfect score:	39	

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2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* A Geneseq 23Sep04:* geneseqp2000s:* geneseqp2001s:* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Aab99759 Rhesus D	Aab99769 Rhesus D	Aau03644 Group B S	Abu21589 Protein e	Abu38334 Protein e	Abu24881 Protein e	Abp30560 Streptoco		Abu29756 Protein e	Adc97241 E. faeciu	Abp26968 Streptoco		Abb55385 Lactococc	Abo74582 Pseudomon	Abu22414 Protein e	Ada49403 Multi-epi	Ado24081 Epigene c	Abo70593 Pseudomon	Abp53931 VEGFR-3 b	Abp53932 VEGFR-3 b	Aao13595 Human pol	Aar15437 Heavy cha	Abo27261 ICAM-1 bi	Abo27269 ICAM-1 bi	Abo27263 ICAM-1 bi
	ID	AAB99759	AAB99769	AAU03644	ABU21589	ABU38334	ABU24881	ABP30560	ABU40245	ABU29756	ADC97241	ABP26968	ABB55389	ABB55385	AB074582	ABU22414	ADA49403	AD024081	ABO70593	ABP53931	ABP53932	AA013595	AAR15437	AB027261	AB027269	AB027263
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ا ع مد	Match	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	87.2	84.6	84.6	84.6	84.6	84.6	84.6	84.6
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## ALIGNMENTS

Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; idiopathic thrombocytopaenic purpura; immunoglobulin. Rhesus D antibody binding peptide SEQ ID NO:4. AAB99759 standard; peptide; 10 AA. (first entry) 21-SEP-2001 AAB99759; RESULT 1 AAB99759 

EP1106625-A1. Homo sapiens

99EP-00122858. 99EP-00122858 17-NOV-1999; 17-NOV-1999; 13-JUN-2001.

(ZLBB-) ZLB BIOPLASMA AG.

WPI; 2001-383568/41.

Miescher S,

Hofmann A, Fisch I;

Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease of the newborn (HDN).

Claim 1; Page 12; 19pp; English.

The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognishing an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are mimotopes which differ in their amino acid sequence from the amino acid

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           properties of Rhesus D protein, and No Peptines No Mill. [I] is used to manufacture an agent for the diagnosis, therapy or prophylaxis of manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. haemolytic diseases of the newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antibodies purified or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes peptides capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (MI) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are
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peptides (V) with immunological
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhesus D antibody binding peptide; Rhesus D; RhD; identification; anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy; prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic; idiopathic thrombocytopaenic purpura; immunoglobulin; circular.
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Pred. No. 9.9;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhesus D antibody related peptide #5.
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sequences of Rhesus D protein; and
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB99769 standard; peptide; 12 AA.
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57.1%;
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Best Local Similarity 57.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-1999;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB99769;
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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mimotopes which differ in their amino acid sequence from the amino acid sequences of Rhesus D protein; and (6) peptides (V) with immunological properties of Rhesus D protein epitopes obtained by (M1). (I) is used to disease associated with Rhesus D antigen, e.g. haemolytic disease of the newborn (HDN) or idiopathic thrombocytopaenic purpura (ITP), for the manufacture of an affinity reagent for anti-Rhesus D antibodies purplied or removed from body fluids or immunoglobulin preparations. Using (I) as an immunogen to raise anti-Rhesus D antibodies avoids using immunisation with foreign erythrocytes thereby avoiding the risk of transmission of viral diseases like AIDS and hepatitis B. The present sequence represents example from the present invention
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus infections, particularly to prevent infection in neonatals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group B Streptococcus, encapsulated bacterium, therapeutic, sepsis,
meningitis, neonate, antigenic, vaccine, infection, genital tract,
capsid polysaccharide vaccination.
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0
                                                                                                                                                                                                                                                                                                                       4; Length 12;
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                                                                                                                                                                                                                                                                                                                     87.2%; Score 34; DB
57.1%; Pred. No. 12;
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU03644 standard; protein; 452 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-2000; 2000WO-GB003437.
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                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                  Sequence 12 AA;
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Matches
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(1) a vector comprising a promiter of a cell. Also included are:

(1) a vector comprising a promiter of a cell. Also included are:

(1) a vector comprising a promiter operably linked to the nucleic acid

choolypeptide whose expression is inhibited by the antisense

nucleic acid; (2) a host cell containing the vector; (3) an isolated

cholypeptide or its fragment whose expression is inhibited by the

antisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

cholypeptide; (5) producing the polypeptide; (6) inhibiting cellular

proliferation or the activity of a gene in an operon required for

the polypeptide; (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

crequired for proliferation, or that inhibits cellular proliferation; (8)

cepthway in which a proliferation required gene or its gene product lies

or a gene on which the test compound that inhibits proliferation of an

organism acts; (9) manufacturing an antibiotic; (10) profilling a

compound's activity; (11) a culture comprising strains in which the gene

product is overexpressed or underexpressed; (12) determining the extent

cowhich each of the strains is present in a culture or collection of

strains; or (13) identifying the target of a compound that inhibits the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                Gaps
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                                   Score 34; DB 4; Length 452;
Pred. No. 3.6e+02;
0; Mismatches 3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #7116.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 49513; 1766pp; English.
                                                                                                                                                                                   ABU21589 standard; protein; 466 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
2S-OCT-2001; 2001US-0032923P.
08-FEB-2002; 2002US-00372851.
06-MAR-2002; 2002US-0362699P.
                                     87.2%;
57.1%;
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                                                                                                                                                                                                                                        19-JUN-2003 (first entry)
                                                  Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                       Burkholderia fungorum.
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Trawick JD,
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N-PSDB; ACA25459.
                                                                                                                  98
                                                                                        1 GYWXXXW 7
                                                                                                                  92 GYWLSAW
           Sequence 452 AA;
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                                     Query Match
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Wall
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of the nucleic acid inhibits proliferation of a cell. Also included are:

of the nucleic acid inhibits proliferation of a cell. Also included are:

encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
                         identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences
proliferation of an organism. The antisense nucleic acids are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.2%; Score 34; DB 6; Length 466; 57.1%; Pred. No. 3.8e+02; ive '0; Mismatches 3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #23861.
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Yamamoto R,
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Matches 4; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 466 AA;
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Wall D,
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ABU38334
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the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for callular proliferation to isolate candidate molecules for rational corrections or proliferation in calls other than S. aureus, S. typhimurium, C. The target prokaryoric essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
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Xu HH;
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Forsyth RA,
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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les 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium botulinum
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200277183-A2.
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Wall D,
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibitied by the artisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for the proliferation or that has an activity against a biological pathway required for proliferation or that inhibits cellular proliferation of an compound that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a pathway in which a proliferation-required gene or its gene product lies or organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, activity; (11) a culture comprising strains in which the gene product is overaxpressed; (12) determining the extent to product is overaxpressed or underexpressed; (12) determining the extent to the which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound discovery programs. Or for screening for monologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. arruginosa. The present sequence is encoded by one of the target prokaryoric essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WY.

C the target proversed for the printed specification, but was obtained in electronic acids are accounted for prolife
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.2%; Score 34; DB 6; Length 474; 57.1%; Pred. No. 3.8e+02; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus polypeptide SEQ ID NO 10296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP30560 standard; protein; 475 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-OCT-2001; 2001WO-GB004789
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 474 AA;
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Tettelin H;
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treptococcus pyogenes), comprising one of 5483 sequences (51), given in the process pyogenes), comprising one of 5483 sequences (51), given in the process pyogenes), comprising one of 5483 sequences (51), given in the process pyogenes), comprising one of 5483 sequences (51), given in the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the pr
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                                                                                        New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Xu HH;
                                                                                                                                                                                                                                      The invention relates to a protein (ABP25413-ABP30895) from group B
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Pred. No. 3.8e+02;
0; Mismatches 3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #25772
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Yamamoto R,
                                                                                                                                                                                           Claim 1; Page 4161; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU40245 standard; protein; 475 AA
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Carr GJ,
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.2%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus proteins
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 GYWLSAW 98
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N-PSDB; ACA44115.
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Best Local Similarity
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                                           N-PSDB; ABN71191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 475 AA;
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Wall D,
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the 613 antisenee sequences given in the specification where expression of the following relates to an isolated of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense concing a polypeptide whose expression is inhibited by the acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for companied for proliferation, (7) identifying a compound that inhibits proliferation (8) identifying a gene required for cellular proliferation or the become companied for cellular proliferation or the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, s activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to operate or underexpressed; (12) determining the extent compound that inhibits proliferation of an organism. The antisense uncleic acids required for cellular proliferation to isolate candidate molecules for rational correlating for homologous mucleic acids acids required for proliferation in cells other than S. aureus, S. typhhmurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target profarryoric essential genes noncleic acids acids required for proliferation in cells other than S. aureus, S. typhhmurium, ce the target profarryoric essential genes proliferation, but was obtained in electronic format directly from WIPO at the sequence as a sequence of the present sequence is encoded by one of the present discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                    The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 6; Length 475; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #15283.
                                                                                        Claim 25; SEQ ID NO 68169; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU29756 standard; protein; 475 AA.
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25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 GYWISAW 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO20027,7183-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU29756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU29756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
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98US-00107532 97US-0051571P 98US-0085598P

Bush D;

2003-799836/75

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New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 6868; 243pp; English
                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                     Doucette-Stamm LA,
                                                                                                                                                                                                                                                                        N-PSDB; ADC93587
                    US6583275-B1.
                                                                                          30-JUN-1998;
                                                                                                                           02-JUL-1997;
                                                                                                                                            14-MAY-1998;
                                                      24-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                    nfection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                  the nucleic acid inhibits proliferation of a cell. Also included are:

the 6213 antisense sequences given in the specification where expression

of the nucleic acid inhibits proliferation of a cell. Also included are:

concluding a polypeptide whose expression is inhibited by the antisense

concloing a polypeptide whose expression is inhibited by the antisense

contisense nucleic acid; (4) an antibody capable of specifically binding

contisense nucleic acid; (4) an antibody capable of specifically binding

contisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

control or the activity of a gene in an operon required for

proliferation, (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

control or proliferation, or that inhibits cellular proliferation; (8)

dentifying a gene required for cellular proliferation of an

confound's activity; (11) aculture or collection of an

confound's activity; (11) aculture compound that inhibits proliferation of an

compound's activity; (11) aculture compound that inhibits the extent

compound's activity; (11) aculture compound that inhibits the

compound's activity; (11) aculture compound that inhibits the

compound's activity; (11) aculture compound that inhibits the

product is overexpressed or underexpressed; (12) determining the extent

compounds; or (13) identifying the target of a compound that inhibits the

confounds; or (13) identifying the target of a compound cidle required

confounds; or (13) identifying the target of a compound cidle are useful for

conduct is overexpressed or underexpressed; (12) determining are useful for

conduct is overexpressed or underexpressed; (12) determining are useful for

conduct is overexpressed or underexpressed; (13) inhibits the

confounds; or (13) identifying the target conduct and order are useful for

conduct is overexpressed or or isolate conduct acids are usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium.
                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid comprising any one of
                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.2%; Score 34; DB 6; Length 475; 57.1%; Pred. No. 3.8e+02; ive 0; Mismatches 3; Indele
                                                                         Ohlsen KL,
Forsyth RA,
                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 57680; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E. faecium protein sequence SEQ ID 6868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC97241 standard; protein; 478 AA.
                                                                         Malone C,
Carr GJ,
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecium.
                                                                         Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYWLSAW 101
                                                                                                                             2003-029926/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                           WPI; 2003-029926,
N-PSDB; ACA33626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-2004
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                                                                         Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SXXXXXXXXXXXXXX
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The invention relates to an isolated nucleic acid derived from
Enterococcus faccium encoding an Enterococcus faccium polypeptide having
One of 10 fully defined sequences given in the (or comprising 40
sequential nucleotides chosen from any of the nucleic acids, its
complement or sequences hybridising to it). Also included are a
recombinant vector comprising the nucleic acid operably linked to
transcription regulatory element, a cell comprising the vector and a
single-stranded probe comprising the nucleic acid. The nucleic acids are
chosen from 364 disclosed sequences encoding 3654 disclosed proteins.
The nucleic acids is useful for diagnosing pathological conditions
cresulting from E. faccium bacterial infection (e.g. urinary tract
infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
infection, and for screening drugs such as agonists and antagonists. The
nucleic acid is useful for recombinant production of Candida albicans
derived peptides or antisense polypeptides. Pharmaceutical compositions
and vaccines containing the nucleic acid are useful for preventing or
treating Enrococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.2%; Score 34; DB 7; I
57.1%; Pred. No. 3.8e+02;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus polypeptide SEQ ID NO 3112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP26968 standard; protein; 479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 57.1 tes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 GYWLSAW 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 478 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP26968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic species. The proteins of the invention are useful for related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at [tp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic
                                                                                                               New nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 5; Length 490; Pred. No. 3.9e+02; 0; Mismatches 3; Indels
                                               Renault P, Ehrlich SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrlich SD
                                                                                                                                                               Claim 6; SEQ ID NO 2091; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID NO 2087; 2504pp; French.
                 (INRG ) INRA INST NAT RECH AGRONOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorokine A, Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB55385 standard; protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis protein arcD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               87.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000; 2000FR-00004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lactis and related species.
                                                                                                                              lactis and related species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                 Sorokine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-043418/06.
                                                                                WPI; 2002-043418/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 GYWLSAW 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR2807446-A1.
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16-MAY-2002
                                                 Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB55385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
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 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઢ
                                                                                                                                                                                                                                                                                                                                                        The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71256 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a streptococcus bample. (I) is used to detect Streptococcus in a composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be manigitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.2%; Score 34; DB 5; Length 479; 57.1%; Pred. No. 3.9e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                               Grandi G,
                                                                                                                                                               Masignani V, Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                Claim 1; Page 3464; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB55389 standard; protein; 490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis protein arcDl.
                                              27-OCT-2000; 2000GB-00026333
24-NOV-2000; 2000GB-00028727
07-MAR-2001; 2001GB-00005640
               29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis, IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                              (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 GYWLSAW 102
                                                                                                                                                                                                               WPI; 2002-352536/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GYWXXXW 7
                                                                                                               (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                              N-PSDB; ABN67599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FR2807446-A1
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16-MAY-2002
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                                                                                                                                                                                  Tettelin H;
                                                                                                                                                               Telford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB55389;
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Gaps

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Length 499; 3; Indels

Score 34; DB 7; Pred. No. 4e+02; 0; Mismatches

h 87.2%; Similarity 57.1%; 4; Conservative

Query Match Best Local Similarity Matches 4; Conserv

Sequence 499 AA;

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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therexpecification as molecular trasques for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as templates for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-Sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for the printed sequence from USPTO at
                                                                                                                                                                                                                                                                               ö
              species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yegurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at the patent of published by the sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
sequence, particularly to identify Lactococcus lactis or related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                    Score 34; DB 5; Length 496;
Pred. No. 4e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                             3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, SEQ ID NO 23328; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa polypeptide #6757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO74582 standard; protein; 499 AA.
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                                                                                                                                                                                                                                      87.2%;
57.1%;
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                        Local Similarity 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-615309/58.
                                                                                                                                                                                                                                                                                                                                                        GYWISAW 99
                                                                                                                                                                                                                                                                                                                     1 GYWXXXW 7
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                                                                                                                                                                                                   Sequence 496 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1999;
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27-JUL-1998;
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Burkholderia mallei.

Protein encoded by Prokaryotic essential gene #7941.

19-JUN-2003 (first entry)

ABU22414;

ABU22414 standard; protein; 506 AA.

RESULT 15

111 GYWISAW 117

1 GYWXXXW 7

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the invention relates to an instruction acts compileration of the nucleic acid inhibits proliferation of a cell. Also included are:

Co the nucleic acid inhibits proliferation of a cell. Also included are:

Co the nucleic acid inhibits proliferation of a cell. Also included are:

Co (1) a vector comprising a promoter operably linked to the nucleic acid

encoding a polypeptide whose expression is inhibited by the antisense

co nucleic acid; (2) a host cell containing the vector; (3) an isolated

co polypeptide or its fragment whose expression is inhibited by the

co proliferation or the activity of a gene in an operon required for

co proliferation or the activity of a gene in an operon required for

co proliferation or that has an activity against a biological pathway or the gene product or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation; (8)

cor a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a

corganism acts; (9) manufacturing an antibiotic; (10) profiling a

compound's activity; (11) a culture comprising strains in which the gene

conduct is overexpressed or underexpressed; (12) determining the extent

conduct is overexpressed or underexpressed; (12) determining the extent

contains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 50338; 1766pp; English.
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Carr GJ,
                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-00815242
                                                                                                                                                                                                                                                                                                                                                         06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
PEB-2002; 2002US-0007281.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACA26284
                                                                                                                                                                                                                    WO200277183-A2.
                                                                                                                                                                                                                                                           03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-)
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segdata.uspto.gov/seguence.html

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proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fix.
                                                                                                                                                                                                                                                                                                                  Sequence 506 AA;
  888888888888888
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Query Match 87.2%; Score 34; DB 6; Length 506; Best Local Similarity 57.1%; Pred. No. 4.1e+02; Matches 4; Conservative 0; Mismatches 3; Indels 124 GYWISAW 130 1 GYWXXXW 7 ઠે

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Gaps °,

Search completed: December 30, 2004, 13:07:56 Job time : 55.6981 Becs

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ORIGINAL SOURCE:
US-09-107-532A-6868
RESULT 1
Sequence 6868, Ap Sequence 19328, A Sequence 18697, A Sequence 9, Appli Sequence 7620, Appli Sequence 172, Appl Sequence 11, Appl Sequence 11, Appl Sequence 16, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 2641, A Sequence 2641, A Sequence 2641, A Sequence 21188, A Sequence 21188, A Sequence 21188, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214, A Sequence 21214,
                                                                                                                                                                                                    December 30, 2004, 12:59:07 ; Search time 18.4151 Seconds (without alignments) 28.810 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/sA_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd
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US-09-252-991A-13338

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US-09-543-681A-7620

US-09-503-610-906-12

US-09-503-610-906-12

US-09-248-796A-15791

US-09-145-828A-11

US-09-145-828A-11

US-09-252-991A-2681

US-09-252-91A-2681

US-09-252-91A-21214

US-09-252-91A-32031

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Sequence 6868, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
1191, Ap
1191, Ap
7233, Ap
7233, Ap
19685, A
22994, A
23312, Ap
8752, Ap
45223, Ap
                                                                                                                                                                                       470, App
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
             US-09-350-841A-1191
US-09-621-976-7633
US-09-621-976-7239
US-09-252-991A-12994
US-09-252-991A-22994
US-09-252-991A-22994
US-09-252-991A-22994
US-09-252-991A-28537
US-09-252-991A-28537
US-09-198-17A-8
US-09-794-51A-8
US-09-794-812-8
US-09-794-812-8
US-09-794-812-8
US-09-794-812-8
US-09-552-868-8
US-09-636-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC
COPERATING SYSTEM: <UNKNOWN>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGRYI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELERAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6868:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: misc_feature
; LOCATION: (B) LÖCATION 1...478
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:
US-09-107-532A-6868
                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 478 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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Sequence 18697, Application US/09252991A

Sequence 18697, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
PAPLICATION:
MICHER OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PILLING DATE: 1099-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18697

LENTH: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PXE International, Inc.
APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
TITLE OF INVENTION: Peeudoxanthoma Elasticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rucations in a gene encoding an ABC transporter (MRP6) causing
Pseudoxanthoma Elasticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 84.6%; Score 33; DB 4; Length 1498; Similarity 57.1%; Pred. No. 6.2e+02; 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 4; Length 543;
Pred. No. 2.6e+02;
0; Mismatches 3; Indels
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Patent No. 6780587
GENERAL INFORMATION:
APPLICANT: PXE International, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene enco
TITLE OF INVENTION: Pseudoxanthoma Elasticu
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2001-02-23
CUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09792616
Patent No. 6780587
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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US-09-792-616-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    960 GYWLSLW 966
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Best Local Similarity
Matches 4; Conserv
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US-09-792-616-9
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US-09-792-616-3
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                                                                                                                                                                                                                                                                                                                                      Sequence 23328, Application US/09252991A

Sequence 23328, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

PAPLICATION: MACLEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

PILE REPERBENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 499
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Pred. No. 2.6e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 499;
                         Score 34; DB 4; Length 478;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 4; Length 499
Pred. No. 1.6e+02;
0; Mismatches 3; Indels
                                                                                       3; Indels
                                                                                    0; Mismatches
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US-09-252-991A-19339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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57.1%;
                            87.2%;
57.1%;
Query Match 87.2
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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RESULT 4

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WS-09-248-796A-15791

| Sequence 15791, Application US/09248796A
| Patent No. 6747137
| Patent No. 6747137
| GENERAL INPORMATION:
| APPLICANT: Keith Weinstock et al
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
| TITLE OF INVENTION: NUMBER: US/09/248,796A
| TITLE OF INVENTION NUMBER: US/09/248,796A
| CURRENT PILING DATE: 1999-02-12
| PRIOR APPLICATION NUMBER: US 60/074,725
| PRIOR APPLICATION NUMBER: US 60/096,409
| PRIOR FILING DATE: 1998-08-13
| NUMBER OF SEQ ID NOS: 28208
| SEQ ID NO 15791
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Pred. No. 2e+02;
0; Mismatches 3; Indel8
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                                            Query Match 82.1%; Score 32; DB 3; Length 252; Best Local Similarity 57.1%; Pred. No. 1.9e+02; Matches 4; Conservative 0; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. 6566066: g2346968
; PUBLICATION INFORMATION:
US-09-610-906-12
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Walker, Michael G. APPLICANT: Volkmuth, Wayne APPLICANT: Volkmuth, Wayne APPLICANT: Klinger, Tod M.; TILE OF INVENTION: AQUAPORIN-8 VARIANT FILE REFERENCE: PC-0012 CIP CURRENT APPLICATION NUMBER: US/09/610,906 CURRENT APPLICATION NUMBER: 09/226,994 PRIOR FILING DATE: 1999-01-07 NUMBER OF SEQ ID NOS: 12 SOFTWARE: PERL PROGram SEQ ID NO 12 LENGTH: 263
                                                                                                                                                                                                                                                      RESULT 9
US-09-610-906-12
; Sequence 12, Application US/09610906
; Patent No. 6566066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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ORGANISM: Rattus norvegicus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Candida albicans
US-09-248-796A-15791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 GYWDFHW 230
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                                                                                                                                         1 GYWXXXW 7
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       US-09-502-653-10
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 7020, Application US/09543681A
Fatent No. 6605709
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
FRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7620
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                                                                                                                                      84.6%; Score 33; DB 4; Length 1503; 57.1%; Pred. No. 6.2e+02;
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                                                                                                                                                                                   3; Indels
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US-09-502-653-10

Sequence 10, Application US/09502653

Patent No. 6331426

GENERAL INFORMATION:

APPLICANT: Clausen, ID Groth

APPLICANT: Clausen, ID Groth

APPLICANT: Schlein, Martin

APPLICANT: Schlein, Martin

APPLICANT: Bech, Lisbeth

APPLICANT: Bech, Lisbeth

APPLICANT: Bech, Lisbeth

APPLICANT: Bech, Lisbeth

CURRENT Bech, Lisbeth

APPLICANT: Bech, Lisbeth

APPLICANT: Bech, Lisbeth

APPLICANT: Bech, Lisbeth

CURRENT APPLICANTON: NOVEL GALACTANASES

FILE REFERENCE: 5481.200-US

CURRENT APPLICATION: NOVEL GALACTANASES

CURRENT APPLICATION: NOVER: PA 1999 00184

EARLIER APPLICATION NUMBER: PA 1999 00799

EARLIER FILING DATE: 1999-06-U7

EARLIER PILING DATE: 1999-06-U7

EARLIER PILING DATE: 1999-06-U7

EARLIER PILING DATE: 1999-06-U7

MUMBER: OF SEQ ID NOS: 52

SEQ ID NO 10

LENGTHARE: PASESQ for Windows Version 3.0

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Proteus mirabilis
                                                                                                                                                         Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
SEQ ID NO 3
LENGTH: 1503
TYPE: PRT
ORGANISM: Homo Bapiens
                                                                                                                                                                                                                                                                           965 GYWLSLW 971
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                                                                                                                                                                                                                                1 GYWXXXW 7
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Matches 4; Conserv
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US-09-543-681A-7620
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                                                                              ; OKGANISM: D.
US-09-792-616-3
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REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)
                                                                Sequence 26841, Application US/09252991A Patent No. 6551795
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Patent No. 5643772
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 GYWGGYW 267
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                                             JS-09-252-991A-26841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-26841
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                                                                                                                                                                                                  APPLICANT: Abbort Laboratories
APPLICANT: Abbort Laboratories
APPLICANT: Abbort Laboratories
APPLICANT: Leonard, Amanda E. Y.
APPLICANT: Hunmond, Jennifer
APPLICANT: Thurmond, Jennifer
APPLICANT: Thurmond, Jennifer
APPLICANT: Atrichmer, Stephen J.
APPLICANT: Parker-Barnes, Jennifer M.
TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
TITLE REFERENCE: 6407.US.01
CURRENT APPLICATION NUMBER: US/09/145,828A
CURRENT APPLICATION NUMBER: 1998-09-02
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 11
LENGTH: 278
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Leonard, Amanda Bun-Yeong
APPLICANT: Hoang, Yung-Sheng
APPLICANT: Hoang, Yung-Sheng
APPLICANT: Hoang, Yung-Sheng
APPLICANT: Hoang, Yung-Sheng
APPLICANT: Horeatra, Suzette L.
TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
FILE REFERENCE: 6407.US.P3
CURRENT APPLICATION NUMBER: US/09/903,456
CURRENT FILING DATE: 2001-07-11
PRIOR PELING DATE: 12000-07-24
PRIOR PLING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR APPLICATION NUMBER: US 09/379,095
PRIOR PILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 278
                                                                                                                                 ; Sequence 11, Application US/09145828A; Patent No. 6403349; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-903-456-18
; Sequence 18, Application US/09903456
; Petent No. 6677145
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
, ORGANISM: Caenorhabditis elegans
US-09-145-828A-11
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Best Local Similarity 57.1%;
Matches 4; Conservative
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||| | GYWPITW 90
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US-09-145-828A-11
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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 339
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TITLE OF INVENTION: POLYPEPTIDES BINDING ANTI-
TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, DNA
TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRID
TITLE OF INVENTION: WECTOR AND TRANSFORMED HOST AND
TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS AND KIT
NUMBER OF SEQUENCES:
OCRRESSPONDENCE S:
ADDRESSE: PHILLIPS, MOORE, LEMPIO & FINLEY
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
COUNTRY: United States of America
ZIP: 94366-1840
COUNTRY: United States of America
ZIP: 9436-1840
COMPUTER: PC
COUNTRY: United States of America
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: HAND DOCALOR OF STATORNEY/AGENT INFORMATION:
DEGRAPHED AND DATE: HAND DATE: HAND DATE: HAND DATES: DEGRALORS.
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RESULT 15
US-09-248-796A-15188

i Sequence 15188, Application US/09248796A

j Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REPERENCE: 107196.132

CURRENT PILING DATE: 1999-02-12

PRIOR PILING DATE: 1999-02-13

PRIOR PELING DATE: 1998-02-13

PRIOR PELING DATE: 1998-06-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15188

LENGTH: 367
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.1%; Score 32; DB 1; Length 362; Best Local Similarity 57.1%; Pred. No. 2.7e+02; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                      NAME/KEY: Positions coded by nonsense codons are NAME/KEY: identified as Xaa.
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TELEPHONE: (415) 324-1677
TELEPHONE: (415) 324-1679
TELEPAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: ORGANISM: CTYPCOSPOXIGIUM PARVUM
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT Candida albicans US-09-248-796A-15188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 GYWWLTW 222
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Sequence

Sequence 273234, Sequence 1, Appli Sequence 5, Appli Sequence 13, Appli Sequence 17, Appl Sequence 27, Appl Sequence 27, Appl Sequence 37, Appl Sequence 37, Appl Sequence 43, Appl Sequence 66, Appl Sequence 66, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 64263, Appl Sequence 642644646464646464646464646646464646

US-10-046-922-34 US-10-046-922-35 US-10-425-115-287762 US-10-425-115-287762 US-09-910-483-15 US-09-910-483-13 US-09-910-483-13 US-09-910-483-13 US-09-910-483-13 US-09-910-483-13 US-09-910-483-13 US-09-910-483-25 US-09-910-483-31 US-09-910-483-31 US-09-910-483-41 US-09-910-483-41 US-09-910-483-41 US-09-910-483-41 US-10-425-115-35518 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-160-222-86 US-10-425-115-35114 US-10-450-022-7 US-10-450-022-7

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Sequence 308836, Application US/10425115
; Sequence 308836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION NUMBER: US/10/425,115
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT PILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 308836
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57.1%; Pred. No. 1.1e+02;
ive 0; Mismatches 3;
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US-10-425-115-308836
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US-10-437-963-176036
Sequence 176036, Application US/10437963
Publication No. US20040123343A1
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Zea mays
GYWGASW
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Sequence 49513, A
Sequence 23291, A
Sequence 66258, A
Sequence 52805, A
Sequence 13733, A
Sequence 57680, A
Sequence 58169, A
Sequence 68169, A
Sequence 69169, A
Sequence 87, Appl
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                                                                                                              December 30, 2004, 13:08:04; Search time 59.6226 Seconds (without alignments) 48.267 Million cell updates/sec
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VS-10-437-963-176036

VS-10-910-007-88

VS-10-282-122A-49513

VS-10-369-493-23291

VS-10-369-493-23291

VS-10-369-493-13733

VS-10-282-122A-58169

VS-10-282-122A-68169

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                GenCore version (c) 1993 - 2004
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Maximum Match 100%
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Match Length
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Perfect score:
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US-10-433-747B-17 US-10-450-185B-2 US-10-450-185B-17 US-10-433-747B-2

ALIGNMENTS

Sequence 9632, Ap Sequence 19811, A Sequence 16537, A

Sequence 199114, Sequence 7, Appli Sequence 4, Appli

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Gaps

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Length 58 Indels

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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10 (52052)B
CURRENT FILING DATE: 2003-02-28
FRICH APPLICATION NUMBER: US 60/360,039
FRICH FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23291
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yanamoro, Kobert
APPLICANT: Yanamoro, Kobert
APPLICANT: Yanamoro, Kobert
APPLICANT: Xu, H.
TITLE REPERBUCE: BLITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/206
FRIOR PELICATION NUMBER: 60/206
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR PLING DATE: 2000-05-26
FRIOR PLING DATE: 2000-05-26
FRIOR PELING DATE: 2000-09-06
FRIOR PLING DATE: 2000-09-06
FRIOR PELING DATE: 2000-09-06
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2000-11-27
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Pred. No. 5.8e+02;
0; Mismatches 3; Indels
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Publication No. US20030233675A1
GENERAL INFORMATION:
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57.1%;
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-369-493-23291
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                      Wall, Daniel
Trawick, Joh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 GYWVSAW 92
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Availc, David K.
APPLICANT: Shou' Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bucharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 176036
LENGTH: 72
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Pred. No. 5.6e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: PAT_MRT4530_73824C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 88, Application US/10091007
| Publication No. US20030170782A1
| GENERAL INFORMATION:
| APPLICANT: Microbial Technics limited APPLICANT: Hanniffy, Sean B
| TILLE OF INVENTION: Proteins | TILLE OF INVENTION: Proteins | FILE REFERENCE: PWC/P21978WO | CURRENT APPLICATION NUMBER: US/10/091,007 | CURRENT FILING DATE: 1999-09-07 | PRIOR PLICATION NUMBER: GB 9921125.2 | PRIOR PLICATION NUMBER: GB 9921125.2 | NUMBER OF SEQ ID NOS: 276 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | SEQ ID NO 88 | 
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Chery1
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-88
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57.1%;
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Best Local Similarity 57.1.
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Oryza sativa
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US-10-282-122A-49513
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Wang, Liangsu
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US-10-369-493-13733
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAR.034

FILE REFERENCE: ELITAR.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 06/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

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PRIOR PLING DATE: 2000-05-36

PRIOR PLING DATE: 2000-05-36

PRIOR PLING DATE: 2000-05-36

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-110-23

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-12-26

PRIOR PLING DATE: 2001-12-26

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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 66258
LENGTH: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 5.8e+02;
Score 34; DB 14; Length 469;
Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3, Indels
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                                                  0; Mismatches
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; Sequence 52805, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                             Sequence 66258, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.2%;
57.1%;
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Liangeu
APPLICANT: Zamwdio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.2
Best Local Similarity 57.1
Matches 4; Conservative
                                                  4; Conservative
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Ouery Match
Best Local Similarity
Matches 4; Conserv
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Sequence 13733, Application US/10369493
; Sequence 13733, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Glodian, Barry S.
; APPLICANT: Ghoman, Barry S.
; APPLICANT: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION WUMBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13733
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tanamoto, Kobert
APPLICANT: Tanamoto, Kobert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT PELLING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/201,078
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR PILING DATE: 2000-05-25
FRIOR APPLICATION NUMBER: 60/206,335
FRIOR PLING DATE: 2000-09-06
FRIOR PLING DATE: 2000-09-06
FRIOR PELLORION NUMBER: 60/230,335
FRIOR PILING DATE: 2000-09-09
FRIOR PELLORION NUMBER: 60/230,337
FRIOR PELLORION NUMBER: 60/230,337
FRIOR PELLORION NUMBER: 60/230,337
FRIOR PELLORION NUMBER: 60/230,337
FRIOR PELLORION NUMBER: 60/230,337
FRIOR PELLORION NUMBER: 60/230,337
FRIOR PELLORION NUMBER: 60/230,337
FRIOR PELLORION NUMBER: 60/253,625
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR PELLING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR PELLING DATE: 2001-02-09
FRIOR PELLING DATE: 2001-02-09
FRIOR PELLING DATE: 2001-02-09
FRIOR PELLING DATE: 2001-02-16
FRIOR PELLING DATE: 2001-02-09
FRIOR PELLING DATE: 2001-02-09
FRIOR PELLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-282-122A-52805
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 57.1
Matches 4; Conservative
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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; ORGANISM: Pseudomonas putida
US-10-282-122A-68169
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 GYWISAW 99
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                               S-10-282-122A-68169
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR PILING DATE: 2000-03-21
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR PILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-06
FRIOR PILING DATE: 2000-09-06
FRIOR PILING DATE: 2000-09-09
FRIOR PILING DATE: 2000-10-23
FRIOR PILING DATE: 2000-10-23
FRIOR PILING DATE: 2000-11-27
FRIOR PILING DATE: 2000-11-27
FRIOR PILING DATE: 2000-11-27
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FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-12-22
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FRIOR FILING DATE: 2001-12-24
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                                                                                                                                                Score 34; DB 14; Length 475;
Pred. No. 5.9e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 57680, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , TYPE: PRT
, ORGANISM: Enterococcus faecium
US-10-282-122A-57680
                                                                                                                                                   87.2%;
57.1%;
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                  4; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserva
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APPLICANY: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPREENCE: ELITAR.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/203,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-110-23

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/263,636

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2000-12-26

PRIOR FILING DATE: 2001-12-29

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-36

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

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PRIOR FILING DATE: 2001-02-09

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PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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US-10-282-122A-50338
Sequence 50338, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
Sequence 68169, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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ORGANISM: Artificial Seguence
                                                      ; FEATURE:
; OTHER INFORMATION: HIV-TC
US-09-894-018-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: HIV-TC
US-10-474-960A-87
                                                                                                                                                                                                                                                                                                                                                                                              22 GYWQATW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GYWQATW 28
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APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT PAPLICANTON NUMBER: 06/191,078
PRIOR PILING DATE: 2000-05-20
PRIOR PILING DATE: 2000-05-20
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR
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Pred. No. 6.2e+02;
0; Mismatches 3; Indels
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Baker, Denisw
APPLICANT: Brown, David
ITLE OF INVENTION: METDOS AND SYSTEM FOR OPTIMIZING
ITLE OF INVENTION: METDOS AND PEPTIDES THEREBY
FILE REPERENCE: 39963-20033.00
CURRENT APPLICATION NUMBER: US 60/278
FRIOR APPLICATION NUMBER: PCT/US00/35568
FRIOR APPLICATION NUMBER: US 60/173,390
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOPTWARE: FASELED fOR Windows Version 4.0
SEQ ID NO 87
LIENGHH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 87, Application US/09894018
Patent No. US20020119127A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Burkholderia mallei
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Best Local Similarity 57.1%;
Matches 4; Conservative
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US-09-894-018-87
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10-09-094-018 INPORMATION: HIV-TC

Ouer, Watch

Dear Vantch

Section 11, 2014, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015, 2015,
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Search completed: December 30, 2004, 13:50:03 Job time : 60.6226 secs

1 GYWXXXW 7

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2 GYWLTIW 8

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December 30, 2004, 12:58:17 ; Search time 9.20755 Seconds (without alignments) 83.598 Million cell updates/sec
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                        US-10-046-922-68
39
1 GYWXXXWX 8
                                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                             Scoring table:
                                                                                                      Run on:
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

283416

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

283416 seqs, 96216763 residues

Searched:

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RIES	Description	hypothetical prote			u	probable amino aci	arginine/ornithine	arginine/ornithine	arginine/ornitine	arginine/ornitine	Ig heavy chain pre	CDPdiacylglycerol	hypothetical prote	oligopeptide ABC t	hypothetical prote	8		cal	д	hypothetical prote	o,	hypothetical prote	_	٠.	_		O3	lysis protein S -	hynotherical prote
SUMMARIES	Ü	T03190	S12193	T37139	D70048	E83497	T46745	JH0110	C86879	G86878	C34903	873905	A69843	G72215	AE2047	C95307	C95282	AI3201	E83268	T15414	B95952	AC2392	AH2975	C98307	T15413	T31037	T42216	\$22905	E69903
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	Length	72	108	345	469	472	475	482	490	497	142	227	250	289	360	441	508	517	519	534	535	541	563	563	592	778	1502	71	83
4	Query Match	87.2	87.2	87.2	87.2		87.2	87.2	87.2	87.2	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	82.1	82.1
	Score	34	34	34	34	34	34	34	34		33		33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	32	33
	Result No.	-	7	e	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		56	27	28

hypothetical prote	nypothetical prote	probable mccF prot	aquaporin 8 - mous	aquaporin 8 - rat	phosphatidate cyti	phosphatidate cyti	probable sugar ABC	protein F41H10.7 [	hypothetical prote	siderophore/Surfac	conserved hypothet	probable secreted	oligopeptide trans	probable ABC trans	hypothetical prote
S76385	D87264	E75325	JC5806	JC5622	F83188	JC4832	H95869	E88690	C82611	H97146	AB0301	T35164	S77572	G95389	B86233
7	~	~	~	~	~	N	7	~	~	7	7	~	7	~	7
218	218	257	261	263	271	271	282	286	344	447	448	466	519	536	631
82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1	82.1
32	32	32	32	32	32	32	32	32	32	32	35	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

 RESULT 1  T03190 hypochetical protein 72B - rice mitochondrion C;Species: mitochondrion Oryza sativa (rice) C;Species: mitochondrion Oryza sativa (rice) C;Species: mitochondrion Oryza sativa (rice) C;Species: mitochondrion Oryza sativa (rice) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004 C;Accession: T03190 R;Itadani, H.; Wakasul, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A. Plant Cell Physiol. 35, 1239-1244, 1994 A;Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existence A;Reference number: 214841; MUID:95211382; PMID:7545979 A;Accession: T03190 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-72 cITA> A;Coss-references: UNIPROT:035302; EMBL:D32052; NID:9769704; PIDN:BAA06811.1; PID:976970 A;Genetice: C;Genetice: C;Genetice: A;Geneme: mitochondrion C;Keywords: mitochondrion
 Query Match Best Local Similarity 57.1%; Pred. No. 15;  Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy 1 GYWXXXW 7  Db 34 GYWSSHW 40
 RESULT 2 S12193 hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1 C;Species: Thiobacillus ferrooxidans C;Species: Thiobacillus ferrooxidans C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004 C;Accession: S12193 R;Drolet, M;, Zanga, P; Lau, P.C.K.
Mol. Microbiol. 4, 1381-1391, 1990 A)Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans j A,Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans j A,Recession: S12193 A,Status: Dreliminary; translation not shown A,Molecule type: DNA A,Residues: 1-108 CDRO> C,Genetics: Cross-references: UNIPROT:P20088; EMBL:X52699; NID:g48158; PIDN:CAA36930.1; PID:g48164 C,Genetics:
 A;Genome: plasmid pTF1 Query Match Best Local Similarity 57.1%; Pred. No. 21; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GYWXXXW 7

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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83497
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br;
R;Stover, C.K.; Pham, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
dman, S.; Yuan, Y. Larbig, K.; Lim,
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                .,,...s: complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:0914E4; GB:AE004549; GB:AE004091; NID:g9947110; PIDN:AAG0458:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Lactobacillus sakei
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C; Accession: T46745
R; Zuniga, M; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, C
J. Bacteriol. 180, 4154-4159, 1998
A; Title: Structural and functional analysis of the gene cluster encoding the enzymes of t
A; Reference number: Z23141; MUID:98361904; PMID:9696763
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C;Date: 3.1-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: JH0110; A8299
R;Luethi, E.; Baur, H.; Gamper, M.; Brunner, F.; Villeval, D.; Mercenier, A.; Haas, D.
A;Title: The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa cont:
A;Reference number: JH0110; MUID:90236296; PMID:2158926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:053092; EMBL:AJ001330; NID:g2764610; PIDN:CAA04686.1; PID:g2?
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: necessary for arginine transport; involved in ornithine-arginine exchange A;Pathway: arginine catabolism C;Superfamily: L-lysine transport protein
                                                                 robable amino acid permease PA1194 [imported] - Pseudomonas aeruginosa (strain PAO1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 2;
Pred. No. 81;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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Pred. No. 81;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Gene: PA1194
C.Superfamily: L-lysine transport protein
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Similarity 57.1%;
4; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-472 <STO>
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C; Function:
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D10048
ABC transporter (amino acid permease) homolog yvsH - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D70048
C;Accession: D70048
C;Brons, S; Brounillet, S; Bruschi, C;V.; Caldwell, B; Capuano, V; Carter, N.M.; Chc
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V.; Berter
C; Brons, S; Brounillet, S; Bruschi, C;V.; Caldwell, B; Capuano, V; Carter, N.M.; Chc
A; Enrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Galler
iech, J; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S; Hosono, S; Hullo, M.F.
Koetter, P; Koningstehl, G; Krogh, S; Kumano, M; Kurita, K.; Lapidus, A; Lardinois,
A;Authors: Lauber, J; Lazarevic, V; Lee, S.M.; Levine, A; Liu, H.; Msauda, S; Maueel
Y, M.; Ogawa, K.; Ogiwara, A; Oudega, B; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E; Roche, B; Rose, M; Sadaie, Y; Scanlon,
A;Authors: Schleich, S.; Schroeter, R; Scoffone, F; Sekiguchi, J; Sekowska, A; Seron
akeuchi, M; Tamakoshi, A.; Tanaka, T; Tarpgtra, P; Tognoni, A; Togato, V; Uchiyama,
T; Wincers, P; Wipat, A.; Yamanoto, H.; Yamane, K.; Yamanoto, K.; Yata, K.; Yoshida, K.;
A;Accession: D70048
A;Accession: D70048
A;Accession: D70048
A;Accession: D70048
A;Accession: D70048
A;Accession: D70048
A;Accession: D70048
A;Accession: D70048
A;Accession: D70048
A;Residues: Ladés «KUN»
A;Accession: D70048
A;Residues: Preliminary; nucleic acid sequence not shown; translation not shown
A;Mesidues: DNA
A;Residues: DNA
A;Residues: Preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: DNA
A;Residues: DNA
                                                                                                                                                                                             hypothetical protein SCJ9A.03c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: 31-8e-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37339
R;Harxis, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Bubmitted to the EMBL Data Library, August 1999
A;Reference number: Z21622
A;Accession: T37339
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-345 < HAR>
A;Residues: 1-345 < HAR>
A;Residues: 1-345 < HAR>
A;Coss-references: UNIPROT: Q9SIR7; EMBL:AL109972; PIDN: CAB53264.1; GSPDB:GN00070; SCOEL
C;Genetics:
A;Gene: SCOEDB:SCJ9A.03c
C;Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c
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Pred. No. 80;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.2%; Score 34; DB 2; Length 345; 57.1%; Pred. No. 61;
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4; Conservative
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||| |
| GYWRSSW 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYWVASW 103
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Best Local Similarity
Matches 4; Conserv
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                                    89
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A, Accession: JH0110

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R.Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Blol. (Chem. 265, 133-138, 1990)
A.F.Ticle: Active site structure and antigen binding properties of idiotypically cross-reach A.R.F. Active site structure and antigen binding properties of idiotypically cross-reach A.Reference number: A34903; MUID:90094387; PMID:2104617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) pgsA - Mycc Species: Mycoplasma pneumoniae  
C;Species: Mycoplasma pneumoniae  
C;Species: Mycoplasma pneumoniae  
C;Species: Mycoplasma pneumoniae  
A;Variety: C29342  
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004  
C;Accession: S73905  
R;Hibert, H;Plagens, H;Pirkl, E;Li, B.C.;Herrmann, R. Nucleic Acids Res. 24, 4420-4449, 1996  
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae  
A;Reference number: S73327; MUID:97105885; PMID:8948633
                           GB:AE005176; PID:g12725079; PIDN:AAK06129.1; GSPDB:Gh
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A;Cross-references: UNIPROT:P75520; EMBL:AE000057; GB:U00089; NID:g1674279; PIDN:AAB96227
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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A,Genetic code: SGC3
C,Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
C,Keywords: transferase
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A,Status: preliminary, nucleic acid sequence not shown, translation not shown
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                          Gaps
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
                                                                                                                                                                                                                  Similarity 57.1%; Score 34; DB 2; Length 497; Similarity 57.1%; Pred. No. 85; 4; Conservative 0; Mismatches 3; Indels
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C, Superfamily: immunoglobulin V region; immunoglobulin homology C, Keywords: heterotetramer; immunoglobulin C; Keywords: heterotetramer; immunoglobulin homology <IMM>
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Pred. No. 40;
0; Mismatches
                    A,Cross-references: UNIPROT:Q9CE19; GB.AEC
A,Experimental source: strain IL1403
C,Genetics:
A;Gene: arcb2
C,Superfamily: L-lysine transport protein
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Best Local Similarity 57.1%;
Matches 4; Conservative (
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Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A, Residues: 1-497 <STO>
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                    A; Residues: 1-482 <LUE>
A; Residues: 1-482 <LUE>
A; Cross-references: UNIPROT: P18275; GB: M33223; NID: GI51030; PIDN: AAA25719.1; PID: GI51031
A; Cross-references: UNIPROT: P18275; GB: M33223; NID: GI51030; PIDN: AAA25719.1; PID: GI51031
A; Note: the gene encoding this protein is located upstream of the arcABC genes which enc R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A; Accession: A82959
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A;Residues: 1-490 <STO>
A;Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:G
A;Experimental source: strain IL1403
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-482 <570>
A,Cross-references: GB:AE004930; GB:AE004091; NID:g9951472; PIDN:AAG08555.1; GSPDB:GN001
A,Experimental source: strain PA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arginine/ornitine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL146 C;Species Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 C;Accession: C86879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86879
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.; Ehrli
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis a Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86878
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Pred. No. 82;
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A,Gene: arcD1
C,Superfamily: L-lysine transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: arcD; PAS170
C;Superfamily: L-lysine transport protein
C;Keywords: transmembrane protein
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Similarity 57.1%;
4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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RESULT 9

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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2047
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A,Residues: 1-360 «KUR»
A,Residues: 1-360 «KUR»
A,Cross-references: UNIPROT:QBYVP3; GB:BA000019; PIDN:BAB73630.1; PID:gl7131021; GSPDB:GP
B,Experimental source: strain PCC 7120
C,Genetics:
A,Gene: all1931
                                                                            hypothetical protein all1931 (imported) - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: December 30, 2004, 13:17:15
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57.1%;
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-441 <KUR>
                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                     A; Accession: AE2047
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                                                                     oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72215
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 199, 123-129, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUD:99287316; PMID:10360571
A;Accession: G72215
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: UNIPROT:Q9X270; GB:AE001813; GB:AE000512; NID:g4982321; PIDN:AAD3681
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-250 «KUN»
A;Cross-references: UNIPROT:031597; GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB12998
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Pred. No. 68;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Experimental source: strain 168
Genetics:
A, Gene: yjbs
C, Superfamily: Bacillus subtilis hypothetical protein yjbA
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Pred. No. 77;
0; Mismatches
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C;Superfamily: oligopeptide permease protein oppB
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probable transport protein SWa0684 [imported] - Sinorhizobium meliloti (strain 1021) mage C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse, F.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Aproc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilots A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: 0922T6; GB: AB: 006469; PIDN: AAK65021.1; PID: 914523451; GSPDB: GA A; Experimental source: strain 1021, megaplasmid pSymA R; Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 200. A; A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C A; Reference number: Asconsolite genome of the legume symbiont Sincrhizobium meliloti.
A; Contents: annotation
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Length 360;
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Pred. No. 1.1e+02;
0; Mismatches 3;
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Score 33; DB;
Pred. No. 94;
0; Mismatches
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Q64dl5 oenococcus
Q64dl5 oenococcus
Q64dl5 bacillus th
Q613£7 bacillus an
Q73dl5 bacillus ac
Q81v71 bacillus ac
Aat29732 bacillus
Q6tk71 streptococc
Q32204 bacillus su
Aat30325 streptoco
Q6tp27 bacillus th
Q73e85 bacillus co
Q6hp27 bacillus co
Q81flb bacillus co
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032816 lactococcus
Q8et30 oceanobacil
06f6u4 acinetobact
Q9slr7 streptomyce
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                                                                                                                December 30, 2004, 12:57:52 ; Search time 73.8113 Seconds (without alignments) 62.362 Million cell updates/sec
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Q811H9
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Q914E4
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Q8DWP9
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                GenCore (c) 1993
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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Perfect score:
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Q9ce19 lactococcus
Q9cs19 lactococcus
Q9cs74 lactococcus
Q7zjj7 human immun
Q7vbg3 prochloroco
Q6nf17 corynebacte
Cae50615 corynebac
Q9ky37 streptomyce
Q9ky37 streptomyce
Q98486 zea mays (m
P75520 mycoplasma
    clostridium
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Itadani H., Makasugi T., Sugita M., Sugiura M., Nakazono M., Hirai A.;
Itadani H., Makasugi T., Sugita M., Sugiura M., Nakazono M., Hirai A.;
"Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:
the existence of many sequences that correspond to parts of
mitochondrial genes in intergenic regions.";
plant Call Physiol. 35:1239-1244(1994).
PIR; T03190; T03190.
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01-JAN-1998 (TrEWBLrel. 05, Last sequence update)
01-JUN-2003 (TrEWBLrel. 24, Last annotation update)
0RF72B.
ORY2a sativa (japonica cultivar-group).
Mitochondrion.
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhhartoideae; Oryzeae; Oryza.
NOBI_TaxID=39947;
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MEDLINE-95308541; PubMed=7788722;
Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiura M.,
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Pred. No. 87;
0; Mismatches 3; Indels
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ARCD_CLOPE
ARCD_PSEAE
Q9CEI5
Q9CEI9
Q9CE19
Q9CE19
Q7CJJ7
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Q9KY37
Q8S486
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Q6NF17
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        4; Conservative
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Gaps

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Indels

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"Frequent detection of escape from cytotoxic T-lymphocyte recognition in perinatal human immunodeficiency virus (HIV) type 1 transmission: the ariel project for the prevention of transmission of HIV from mother to infant.";

J. Virol. 73:3975-3985(1999).
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MEDLINE=97369814; PubNed=9226255;
MEDLINE=97369814; PubNed=9226255;
Duwat P., Cochu A., Bhrlich S.D., Gruss A.;
"Characterization of Lactococcus lactis UV-sensitive mutants obtained by ISS1 transposition.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.2%; Score 34; DB 2; Length 236
57.1%; Pred. No. 2.5e+02;
tive 0; Mismatches 3; Indels
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236 AA; 27062 MW; 24D6BB0409A80BB8 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                          236 AA.
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   Mismatches
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01-JAN-1998 (TrEMBLrel. 05, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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InterPro; IPR010659; RVT connect.
InterPro; IPR010661; RVT thumb.
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Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
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(TrEMBLrel. 12, I
(TrEMBLrel. 26, I
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4; Conservative
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                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                           Polyprotein (Fragment)
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Walker B.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
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                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
Acidithiobacillaceae; Acidithiobacillus.
NCBI_TaxID=920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drolet M., Zanga P., Lau P.C.K.;
"The mobilization and origin of transfer regions of a Thiobacillus
ferrooxidans plasmid: relatedeness to plasmids RSF1010 and pSC101.";
Mol. Microbiol. 4:1381-1391(1990).
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.2%; Score 34; DB 2; Length 130; 57.1%; Pred. No. 1.5e+02;
                                                                                 01-FEE-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 140, Last annotation update)
Hypothetical 12.3 kDa protein in mobl 3'region (ORF 4).
Thiobacillus ferrooxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Briat, 812193; 812193.
PIR; 812193; 812193.
Hypothetical protein; Plasmid.
SECUENCE 108 AA; 12335 MW; A8E67717C109A57E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 AA; 14024 MW; EE0F4A997FCA8CD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible Adenoviral fiber protein (Repeat/shaf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AA.
                               108 AA
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 33020;
MEDLINE=91125140; PubMed=2280689;
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EMBL; BX572092; CAE19526.1; -.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52699; CAA36930.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=PMM1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYWRSSW 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GYWXXXW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=59919;
                                                                                                                                                                                                                                              Plasmid pTF:
                               THIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
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                               YML2 THI
P20088;
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Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S., Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P., Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.; "Unique features revealed by the genome sequence of Acinetobacter sp. ADPI, a versatile and naturally transformation competent bacterium.") Nucleic Acids Res. 0:00(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the model actinomycete Streptomyces
         Bactería; Proteobactería; Gammaproteobactería; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.2%; Score 34; DB 2; Length 333
57.1%; Pred. No. 3.58+02;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome; Hypothetical protein.
SEQUENCE 345 AA; 36929 MW; 23643009936285B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 AA; 36530 MW; 7C887F5127A40682 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09SIR7;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SC00224.
OrderedLocusNames=SC00224; ORFNames=SCJ9A.03c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 345 AA.
                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR002657; BILAC/Na_symport.
Pfam; PF01758; SBF; 1.
Complete proteome.
SEQUENCE 333 AA; 36530 MW; 7C887F5
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EMBL; AL939104; CAB53264.1; -.
PIR; T37139; T37139.
                                     Moraxellaceae; Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.1.
                                                                                                                                                                                                                                                                                                                                   EMBL; CR543861; CAG70223.
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 GYWASRW 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 GYWAARW 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GYWXXXW 7
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                                                                                                                             SEQUENCE FROM N.A.
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Q9KGV3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
Q9KGV3
ID Q9KG
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Q9S1R7
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDILTRE=2220767; PubMed=12235376;
MEDILTRE=2220767; PubMed=12235376;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
Nucleic Acids Res. 30:3927-3935(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transporter; putative sodium/bile acid transporter family
J. Bacteriol. 179:4473-4479 (1997).

EMBL; UB1991; AAC45504.1; -.

GO; GO:0016021; C.integral to membrane; IEA.

GO; GO:00162279; F.amino acid-polyamine transporter activity; IEA.

GO; GO:0006865; P.amino acid transport; IEA.

InterPro; IRR002293; AA/rel_permease1.

Transmembrane.

NON TER 253 253

SEQÜENCE 253 AA; 26569 MW; ICB8FAEF6C38FBB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.2%; Score 34; DB 2; Length 294; 57.1%; Pred. No. 3.1e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                       Score 34; DB 2; Length 253; Pred. No. 2.7e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome; Transmembrane; Transport.
SEQUENCE 294 AA; 31323 MW; F75E50F22EA4071A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Acinetobacter sp. (strain ADP1).
                                                                                                                                                                                                                                                                                                       87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABC transporter permease. OrderedLocusNames=OB0434;
                                                                                                                                                                                                                                                                                                                                         Local Similarity 57.1 nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 GYWLSAW 99
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GYWXXXW 7
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Suchardson P., Rubin B., Tice H.; Suchardson P., Rubin B., Tice H.; Sucharted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AE017355; AAT6241.; -.

InterPro; IPR002293; AA/rel_permeasel.

InterPro; IPR004841; Permease_region.

Pfam, PF00324; AA_permease; 1.

Transmembrane; Transport.

SSQUENCE 465 AA; 50153 MW; 534F03BC0A379E04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R. Richardson P., Rubin B., Tice H.;
Submitted (JAN. 2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AE017225, AAT52924.1;
InterPro; IPR002293; AA/rel permeasel.
InterPro; IPR004841; Permease region.

Frams Pro0324; AA permease region.

Transmembrane; Transport.
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                                                                                                                                                                                                                             05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Probable arginine/ornithine antiporter protein.
Name=arcD, ORFNames=BT9727_0540;
Bacillus thuringlensis serovar konkukian str. 97-27.
Bacteria, Firmicutes; Bacillales; Bacillus;
Bacillus thuringiensis serovar konkukian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Amino acid permease family protein.
                                                                                                                                                                                     465 AA.
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                                                      94 GYWLSSW 100
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  1 GYWXXXW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=281309;
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                                                                                                                                 RESULT 11
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MEDLLNE=22519909; PubMed=12631210;
Divol B., Tonon T., Morichon S., Gindreau E., Lonvaud-Funel A.;
"Molecular characterization of Oenococcus oeni genes encoding proteins
                                                                                                      Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBL TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Note 1.-82, Weimer B., Xie Y.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF282249; AAF86987.1;

EMBL; AF282249; Famino acid-polyamine transporter activity; IEA.

GO; GO:0006851; Famino acid transport; IEA.

GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involved in arginine transport.";
J. Appl. Macrobiol. 94:738-746(2003).
EMBL; AF$41253; AA083382.1,
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid-polyamine transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.2%; Score 34; DB 2; Length 459; 57.1%; Pred. No. 4.6e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                              STRAIN=ML3;
Chou L., Weimer B., Xie Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR002293; AA/rel_permeasel.
Interpro; IPR004841; Permease_region.
Pfam, PR00324; AA_permease; 1.
Transnembrane; Transport.
SEQUENCE 459 AA; 49146 MW; 9718P27B7B937242 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 AA; 50557 MW; 1C6EE79AFF9F8B84 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Arginine/ornithine antiporter Arcb2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oenococcus oeni (Leuconostoc oenos).
Bacteria; Firmicutes; Lactobacillales; Oenococcus.
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GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel_permease1.
InterPro; IPR004841; Permease region.
Pfam; PF00324; AA_permease; 1.
Transmembrane; Transport.
Transmembrane; Transport.
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50040 MW; 9750B5D1019142F2 CRC64;

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Query Match 87.2%; Score 34; DB 2; Length 465; Best Local Similarity 57.1%; Pred. No. 4.7e+02; Matches 4; Conservative 0; Mismatches 3; Indels
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465 AA;
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SEQUENCE
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Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.B., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.; "The genome sequence of Bacillus cereus ATCC 10997 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1."; Nucleic Acids Res. 32:977-988(2004).
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GO:0016021; C:integral to membrane; IEA.
GO:0005279; P:amino acid-polyamine transporter activity; IEA.
GO:0006865; P:amino acid transport; IEA.
GO:0006810; P:transport; IEA.
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Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                          Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome; Transmembrane; Transport. SEQUENCE 465 AA; 50193 MW; C18384E10EBC639D CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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InterPro; IPR002293; AA/rel_permeasel.
InterPro; IPR004841; Permease_region.
Pfam; PF00324; AA permease_region.
Transmembrane; Transport.
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InterPro; IPR002293; AA/rel_permeasel.
InterPro; IPR004841; Permease_region.
Pfam; PP00324; AA_permease;
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Best Local Similarity 57...
Best 4; Conservative
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96 GYWAANW 102
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A Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
A Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
A Holzapple B.K., Oketea O.A., Helgason E., Riletone J., Wu M.,
A Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
A Beboy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
A Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weldman J.F.,
A Bazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
A Hanna P.C., Kolstoe A.-B., Fraser C.M.;
The genome sequence of Bacillus anthracis Ames and comparison to
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GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Fed
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017026; AAP24646.1; -.
TIGR; BA0629; -.
                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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AA; 50250 MW; AA04D53505386FA9 CRC64;
                                                                                                                                                                              091771; O6KX71;
01-UJN-2003 (TERBLE-1. 24, Created)
01-UJN-2003 (TERBLE-1. 24, Last sequence update)
01-OCT-2004 (TERBLE-1. 28, Last annotation update)
                                                                                                                                                                                                                                                                                         Amino acid permease family protein.
OrderedLocusNames=BA0629; ORFNames=GBAA0629;
Bacillus anthracis.
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InterPro; IPR004841; Permease_region.
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Best Local Similarity 57.1%;
Matches 4; Conservative (
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96 GYWAANW 102
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GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  OM protein - protein search, using sw model  Run on: December 29, 2004, 21:02:29; Search time 148 Seconds (without alignments)  19.391 Million cell updates/sec  Title: US-10-046-922-32  Perfect score: 8 Sequence: 1 XXXXXXXX 8 Sequence: 1 XXXXXXXX 8 Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5 Searched: 2002273 seqs, 358729299 residues Total number of hits satisfying chosen parameters: 153769	Minimum DB seq length: 0 Maximum DB seq length: 8 Post-processing: Minimum Match 0* Maximum Match 100* Listing first 45 summaries	Database: A_Geneseq_21Sep04:*  1: geneseqp1980s:* 2: geneseqp1990s:* 3: geneseqp2000s:* 6: geneseqp2001s:* 7: geneseqp2001s:* 8: geneseqp2001s:* 8: geneseqp2004s:* 8: geneseqp2004s:* and is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  **  SUMMARIES  **  Result  Query	No. Score Match Length DB ID   Description

Matches

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RESULT 2 ADD94992

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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
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                                             Platelet aggregation inhibitor peptide #135.
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
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The invention describes peptides of amino acid sequence (1) and their salts. (1) are useful as platelet aggregation inhibitores and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (1) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
defined)"
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                                                                                                                                                                                                                                                     Platelet aggregation inhibitor peptide #145.
 Pred. No. 0;
0; Mismatches
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Query Match

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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guandidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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tive 0; Mismatches
Disclosure; Page 10; 34pp; Japanese.
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                                                                                                                                        New RGD peptide(8) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
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                                                                                           Takiguchi Y;
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0; Mismatches
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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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defined)"
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              platelet aggregation inhibitor; guanidino group; amidino group.
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                                                                                                                                                                                                          Platelet aggregation inhibitor peptide #133.
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 10; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                 ADD94991 standard; peptide; 1 AA.
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Best Local Similarity 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-060950/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (YAWA ) NIPPON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1 AA;
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Modified-site
                                        1 R 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1994;
            1 X 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-1993;
                                                                                                                                                                                                                                                                    Unidentified
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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
                                                                                                                                             Score 0; DB 2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                        completed: December 29, 2004, 21:18:58
                                                                                                                                             Query Match 0.0%;
Best Local Similarity 0.0%;
Matches 0; Conservative
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                                                                                                                                                                                                                   The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.
                                                                                                                                               New RGD peptide (s) useful as anti-platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= OTHER
/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
defined)"
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                                                                                        Takiguchi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Platelet aggregation inhibitor peptide #142.
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                                                                                                                                                                                       Disclosure; Page 10; 34pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD95000 standard; peptide; 1 AA.
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                                                                                         Katada J,
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                                                                                        Sato Y, Hayashi Y,
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/07/820,154A

PILING DATE: 19920113

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

TELEPRAK: (212) 977-9550

TELEPRAK: (212) 664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 121, Application US/07820154A
; Patent No. 5382425
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 40
; NUMBER OF SEQUENCES: 4
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
US-08-801-092-10

US-08-801-092-17

US-08-801-092-34

US-08-801-092-38

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US-09-298-017-25

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Matches

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: New York
COUNTRY: USA
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                                                                                                                                                                           December 29, 2004, 21:10:45; Search time 36 Seconds (without alignments) 14.737 Million cell updates/sec
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                              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Result No.

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0.0%; E
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Best Local Similarity 0.0%
Matches 0; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-213D-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                               APPLICANT: MORIBHTA, Hideaki
APPLICANT: MORIBHTA, Hideaki
APPLICANT: MOBUHARA, Masahirot
APPLICANT: NOBUHARA, Masahirot
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE
TITLE OF INVENTION: SAME AND PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
TITLE OF INVENTION: TREATING USING THE SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYPEPTIDE, DNA FRAGMENT ENCODING THE SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME SAME AND PROCESS, DRUG COMPOSITION AND METHODS OF TREATING USING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUNTRY: Virginia

COUNTRY: United States

COUNTRY: United States

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEFRAX: (703) 836-620
TELEFRAX: (703) 836-2021
SISQUENCE CHARACTERISTICS:
TENGRATION FOR SEQ ID NO: 24:
SISQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCRMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHRAA, Masahinori
TITLE OF INVENTION: SAME AND PROCESS FOR PRODU
TITLE OF INVENTION: INHIBITION PROCESS, DRUG CI
TITLE OF INVENTION: TRAFAING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE:
ADDRESSEE: ADDRESSEE:
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ADDRESSEE: ADDRESSEE:
ADDRESSEE: ADDRESSEE:
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0.0%; Score 0; DB 1

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches
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US-07-791-213D-40
; Sequence 40, Application US/07791213D
; Patent No. 5408895
Sequence 24, Application US/07791213D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                          Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 C 1
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STATE:
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Gaps
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US-08-174-365A-57
US-08-174-365A-57
Sequence 57, Application US/08174365A
Patent No. 5478809
GENERAL INFORMATION:
APPLICANT: Selichi TANIDA et al.
TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FLISG PAPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FLING DATE: 13-NOV-1991
CLASSIFICATION NUMBER: US/07/791,213D
FRING APPLICATION NUMBER: US/07/791,213D
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REFERENCE/DOCKET NUMBER: 029650-032
TELECHOMMINICATION INFORMATION:
TELECHOME: (703) 836-620
TELEFRAK: (703) 836-620
TELEFRAK: (703) 836-2021
INFORMATION FOR SEQ ID NO: 40: SEQUIBLE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Weahington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005 COMPUTER: Laboration STREET: MEDIUM TYPE: Diskette, 3.5 inch, 144 mb COMPUTER: Lab Compatible COMPUTER: Lab Compatible COMPUTER: Wastem: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/174,365A FILING DATE: December 28, 1993 CLASSIFICATION NUMBER: US/08/174,365A FILING DATE: December 28, 1993 FILING DATE: APPLICATION NUMBER: MS-DOS CLASSIFICATION NUMBER: MS-DOS CLASSIFICATION NUMBER: MS-DOS CLASSIFICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: MS-DISK-DATE: APPLICATION NUMBER: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DATE: MS-DISK-DAT
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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; INDIVIDUAL ISOLATE: peptide fragment used in the claims US-07-789-913-23
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                Query Match
Best Local Similarity 0.0%
Occupantive
Occupantive
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Best Local Similarity 0.0%
Matches 0; Conservative
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      ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
OTHER INFORMATION: /note = "Xaa is modified amino acid as
OTHER INFORMATION: described in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/07789913

Patent No. 5559095

GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Fox, James A.
APPLICANT: Pox, James A.
APPLICANT: Vatentino, Karen L.
APPLICANT: Watentino, Monald H.
TITLE OF INVENTION: Ischemia-Related Neuronal Damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1; . 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
CORRENT MING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/07/789,913
FLING DATE: 19911112
CLASSIFICATION NUMBER: US 07/789,713
APPLICATION NUMBER: US 07/789,713
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTONEY/AGENT IRFORMATION:
ANDER COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE COMPUTER OF THE
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
0.0%; Score 0; DB 1
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches
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REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 1 amino acids
                                                                                                                                                                                                   NAME/KEY: modified site
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acid
                              LENGTH: 1 amino acid
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-07-789-913-23
                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Gaps
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                                                                                                                                                                                                                               APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: Ischemia-Related Neuronal Damage NUMBER OF SEQUENCES: 28
CORRESSONDENCE ADDRESS:
ADDRESSEE: Law Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide fragment used in the claims
                                             1; Indels
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  Length 1;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AMG-1990
FILING DATE: 12-NOV-198
FILING DATE: 22-NOV-198
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELERPHONE: (415) 324-0880
DB 1;
0;
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0.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
Score 0; DB 1;
Pred. No. 0;
0; Mismatches
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Patent No. 5559095
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Sreekrishna, Kotikanyadan
APPLICANT: Barr, Kathryn A.
APPLICANT: Barr, Kathryn A.
APPLICANT: Brierley, Russell A.
APPLICANT: Thill, Gregory P.
APPLICANT: Tschopp, Juerg F.
APPLICANT: Tschopp, Juerg F.
TITLE OF INVENTION: PICHIA PASTORIS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONOPEPTIDE GROUP 1 FRAGMENT, PAGE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
             TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA NUMBER OF SEQUENCES: 34
CORRESPONDENCES: AN Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 0; DB 1; Length 1;
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400 Garden City Plaza
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Patent No. 5707828
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0.0%; E
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 0.0%
Matches 0; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                94306
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APPLICANT:
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                                                                                                                                                           APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONOPEPTIDE GROUP 1 FRAGMENT, PAGE 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.0%; Score 0; DB 1;
0.0%; Pred. No. 0;
tive 0; Mismatches
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REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
RECISTRATION NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
                                                                                                         Sequence 23, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SINGH, TEJINDER
GOHIL, KISHOR C
VALENTINO, KAREN L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 0.04
Matches 0; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                    Palo Alto
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US-08-049-794-25
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APPLICANT:
APPLICANT:
                                                                                        US-08-049-794-23
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; Sequence 24, Application US/08293150A
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
      (202)331-7111
                                                                                                                                                                                                                                0.0%;
                   TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 0.00
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Best Local Similarity 0.04
Matches 0; Conservative
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                                                                                                                                        MOLECULE TYPE: peptide US-08-448-606-4
                                                                                      1 amino acid
                                                                                                       amino acid
                                                                                                                                                                                                                                                                                             1 X 1
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US-08-293-150A-24
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                                                                                                         TYPE:
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Patent No. 572114
GENERAL INFORMATION:
APPLICANT: Abrahams n, Lars
APPLICANT: Holmgren, Brik
APPLICANT: Holmgren, Brik
APPLICANT: Mikaelsson, sa
APPLICANT: Mikaelsson, sa
APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
TITLE OF INVENTION: Apolipoprotein AI-M
MINDER OF INVENTION: Apolipoprotein AI-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1;
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CUDNIKKI: U.S.
CUDNIKKI: U.S.
CUDNIKKI: U.S.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIPICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATORNEY/AGENT INFORMATION:
NAME: AMERICK, BUTCON A.
REGISTRATION NUMBER: 24,852
REGISTRATION NUMBER: 24,852
REGISTRATION NUMBER: 24,852
REGISTRATION NUMBER: 24,852
                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 0; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: TOWNERS OF SEQUENCES: TOWNESS: ADDRESS: Pollock, Vande Sande & Priddy STREET: 1990 M Street, N.W., Suite 800 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
U.0%; C.C. No. 0;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 91082
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEG ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                       OPERATING SYSTEM:
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. U.S.
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APPLICANT: KINET. Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
TITLE OF INVENTION: IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
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                                     1; Indels
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Pred. No. 0;
0; Mismatches 1; Indele
Score 0; DB 1; Length 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: VA
COUNTRY: USA
ZUD: 22313-2259
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: 80014
                 Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                       Sequence 16, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
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us-10-046-922-32.8max.rai

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Score 0; DB 1;
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SUFTWARE: PERSESPO for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Patent No. 5795864
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0%
Virginia
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.0
Best Local Similarity 0.0%
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                            22313-1404
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STATE: V
COUNTRY:
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                                                             APPLICANT: KANAMORI, TOSHINOTI

APPLICANT: KANAMORI, TOSHINOTI

TITLE OF INVENTION: POLYEPTIDE, DNA FRAGMENT ENCODING THE

TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME

TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF

TITLE OF INVENTION: TREATING USING THE SAME

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

STREET: P.O. BOX 1404

CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                           CITY: Alexandria
STATE: Virginia
CONTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRET: APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 386,607
REFERENCE/DOCKET NUMBER: 386,607
REFERENCE/DOCKET NUMBER: 386,600
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Pred. No. 0;
0; Mismatches
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; Patent No. 5792629
; GENERAL INFORMATION:
                         GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 0.0*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
    Patent No. 5792629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-293-150A-40
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ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/39,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
ATPONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,607
REGISTRATION NUMBER: 36,607
REGISTRATION NUMBER: 36,607
REGISTRATION NUMBER: 36,607
REGISTRATION NUMBER: 36,607
REGISTRATION NUMBER: 36,607
RELEFANCE/LOCKET NUMBER: 029650-049
TELEFANCE/LOCKET NUMBER: 36,620
TELEFANCE/LOCKET NUMBER: 36,620
TELEFANCE/LOCKET NUMBER: 36,620
TELEFANCE/LOCKET NUMBER: 36,620
TELEFANCE/LOCKET NUMBER: 36,620
TELEFANCE/LOCKET NUMBER: 36,620
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Best Local Similarity 0.0%
Matches 0; Conservative
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0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indel
REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0009.31

TELECPHONE: 650-324-0880

TELEPHONE: 650-324-0860

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acids
TYPE: amino acids
HYPOTHETICAL: NO
ORIGINAL SOURCE:
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SIGNAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
US-08-496-847-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
HYPOTHERICAL: NO
HYPOTHERICAL: NO
HYPOTHERICAL: SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTEY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-TELECOMNUNCATION INFORMATION:
TELEPLAX: 650-324-0800
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
3Y: linear
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0.0%; Score 0; DB 1; Length 1;

Query Match

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Best Local Similarity 0.0%; Pred, No. 0; Mamatches 1; Indels 0; Caps Oy 1 X 1
Db 1 R 1
Search completed: December 29, 2004, 21:20:23
Job time : 37 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	
OM protein - protein search, using sw model	
Run on: December 29, 2004, 21:16:31 ; Search time 137 Seconds (without alignments) 21:006 Million cell updates/sec	
Title: US-10-046-922-32 Perfect score: 8 Sequence: 1 XXXXXXXX 8	
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched: 1599051 seqs, 359727711 residues	
Total number of hits satisfying chosen parameters: 83711	
Minimum DB seq length: 0 Maximum DB seq length: 8	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Pred. No. is the number of results predicted by chance to have a	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Appli	Appli	Appli	Appli	Appli	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
	Ĕ	5,	4	6	4,	6	11,	19,	31,	35,	37,	46,	69	80,
	Description	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
		!												
SUMMARIES	ΩΙ	US-09-778-885-5	JS-09-909-348-4	S-09-982-172-3	JS-09-982-172-4	S-09-982-172-9	US-09-982-172-11	S-09-982-172-19	JS-09-982-172-31	JS-09-982-172-35	JS-09-982-172-37	S-09-982-172-46	US-09-982-172-69	JS-09-982-172-80
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	Query Watch Length DB	-	7	7	7	1	1	-	1	-	-	н	н	н
من	Query Match	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Score	0	0	0	0	0	0	0	0	0	0	0	0	0
	Result No.	-	7	٣	4	2	9	7	8	0	10	11	12	13

Sequence 81, Appl Sequence 83, Appl Sequence 86, Appl Sequence 95, Appl Sequence 112, App Sequence 112, App Sequence 112, App Sequence 113, App Sequence 173, App Sequence 173, App Sequence 190, App Sequence 191, App Sequence 191, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 112, App Sequence 112, App Sequence 113, App Sequence 114, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 116
1 9 US-09-982-172-81 1 9 US-09-982-172-86 1 9 US-09-982-172-95 1 9 US-09-982-172-95 1 9 US-09-982-172-95 1 9 US-09-982-172-106 1 9 US-09-982-172-120 1 9 US-09-982-172-120 1 9 US-09-982-172-120 1 9 US-09-982-172-149 1 9 US-09-982-172-149 1 9 US-09-982-172-160 1 9 US-09-982-172-160 1 9 US-09-982-172-160 1 9 US-09-982-172-100 1 9 US-09-982-172-100 1 9 US-09-982-172-100 1 9 US-09-982-172-100 1 9 US-09-982-172-100 1 9 US-09-982-172-100 1 1 US-09-982-172-100 1 1 US-09-982-172-101 1 1 US-09-982-172-101 1 1 US-09-882-171-611 1 1 US-09-883-245-184 1 1 US-09-883-245-184 1 1 US-09-883-245-184 1 1 US-09-883-245-184 1 1 US-09-883-245-184 1 1 US-09-883-245-184 1 1 US-09-883-245-184
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

```
APPLICANT: Crowther, Roger S.
APPLICANT: Stiernberg, Janet
APPLICANT: Stiernberg, Janet
APPLICANT: Stiernberg, Janet
APPLICANT: Bergmann, John
TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists
TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Rec
TILE REFERENCE: 3033.1003-001
CURRENT PILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/219,800
PRIOR APPLICATION NUMBER: US 60/219,800
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
APPLICANT: Emil Israel Katz
APPLICANT: Emil Israel Katz
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT:
TITLE OF INVENTION: UTILIZING EACH
FILE REPERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide fragment of Thrombin
NAME/KEY: VARIANT
LOCATION:
OTHER INFORMATION: Xaa at position six is Glu or Gln
OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His US-09-909-148-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 0; DB 9;
Pred. No. 0;
0; Mismatches
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09982172 Patent No. US20020137119A1
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Best Local Similarity 0.0%; F
Matches 0; Conservative (
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Best Local Similarity 0.0%;
Matches 0; Conservative
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LOCATION: (25)...(25)
1 LOCATION: (25)... (25)
1 UCCATION: (25)... (25)
US-09-778-885-5
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OTHER INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or Val
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OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (16)...(16)
OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cys, Glu, His or Tyr
                                                                               NAME/KEY: VARIANT
LOCATION: (6)...(6)
OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr
OTHER INFORMATION: or Met
NAME/KEY: VARIANT
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu,
OTHER INFORMATION: Met, Phe or Trp
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DTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr
DTHER INFORMATION: and Ser
                 LOCATION: (5)...(5) OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe, OTHER INFORMATION: Ser, Thr or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gly, His
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OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (11)...(11)
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His,
OTHER INFORMATION: Pro, Trp and Val
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OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
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DIHER INFORMATION: Xaa is any residue except Ala, Asp, Cys,
DIHER INFORMATION: Met, Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATION: (13)...(13)
THER INFORMATION: Xaa is any residue except Asp, Cys, Glu,
THER INFORMATION: or Trp
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OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala
NAME/KEY: VARIANT
LOCATION: (19)...(19)
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DTHER INFORMATION: Xaa is any residue except Arg, Asn,
DTHER INFORMATION: Ser, Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COCATION: (17)...(17)

THER INFORMATION: Xaa is Phe, Tyr, Ile, Trp or Leu
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OTHER INFORMATION: Xaa is any residue except Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.0%; Score 0; DB 9; Best Local Similarity 0.0%; Pred. No. 0; Matches 0; Conservative 0; Mismatches
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OTHER INFORMATION: Xaa is Lys, Asn, Ser or Asp
                                                                                                                                                                                                                                                                                                        JOCATION: (8)...(8)
JTHER INFORMATION: Xaa is Gly or Glu
AAME/KEY: VARIANT
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OTHER INFORMATION: Xaa is Tyr or Phe
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NAME/KEY: VARIANT
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GENERAL INFORMATION:
APPLICANT: Emil lsreel Katz
 REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: UTILIZING EACH
FILE REPERENCE: 01/22283
CURRENT FILING DATE: 2001-10-19
KUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
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APPLICANT: Emil 1srael Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING BACH
FILE REPRENENCE: 01/2283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT APPLICATION DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PATENTION OF SEG ID NOS: 253
SOFTWARE: PATENTION OF SEG ID NOS: 253
LENGTH: 1
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                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-19
                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.0%; Score 0; DB 9; Best Local Similarity 0.0%; Pred. No. 0; Matches 0; Conservative 0; Mismatches
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TITLE OF INVENTION: UTILIZING EACH FILE REFERENCE: 0.1/22283 CURRENT APPLICATION NUMBER: US/09/982,172 CURRENT FILING DATE: 2001-10-19 NUMBER OF SEQ ID NOS: 253 SOFTWARE: Patentin version 3.1 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09982172 Patent No. US20020137119A1
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Patent No. US20020137119A1
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
FEATURE:
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US-09-982-172-31
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                                                                                                 US-09-982-172;4

Sequence 4, Application US/09982172

Patent No. US20020137119A1

GENERAL INFORMATION:

APPLICANT: Emil lerael Katz

TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

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TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

STORMENT APPLICATION NUMBER: US/09/982,172

NUMBER OF SEQ ID NOS: 253

SEQ ID NOS: 253

SED ID NO 4
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Batent No. US20020137119A1

GENERAL INFORMATION:

ABLIGANT: Emil Israel Katz

TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

FILE REPERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT PILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: Patentin version 3.1
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Patent No. US2002013711941
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
ITILE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
ITILE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT
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0.0%; Pred. No. 0;
vative 0; Mismatches 1; Indel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-4
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ORGANISM: Artificial sequence
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Best Local Similarity 0.0*
Matches 0; Conservative
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US-09-982-172-11
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Sequence 46, Application US/09982172

Batent No. US20020137119A1

GENERAL INFORMATION:

APPLICANT: Emil Israel Katz

APPLICANT: Emil Israel Katz

TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT

TITLE OF INVENTION: UTILIZING BACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Emil Israel Katz
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/2283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 69
LENGTH: 1
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Patent No. US20020137119A1

GENERAL INFORMATION:

APPLICANT: Emil Israel Katz

TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI

TITLE OF INVENTION: UTLLIZING EACH

FILE REFERENCE: 01/22283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-46
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Patent No. US20020137119A1
GENERAL INFORMATION:
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APPLICANT: Emil Israel Katz

APPLICANT: Emil Israel Katz

TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UNBER: US/09/982,172

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 35
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Sequence 37, Application Us/09982172

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT PILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
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; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-31
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US-09-982-172-37
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
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ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
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Patent No. US2002013711941

GENERAL INFORMATION:
FALL INFORMATION:
FILLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UNBER: US/09/982,172
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO
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US-09-982-172-83

US-09-982-172-83

US-09-982-172-83

Sequence 83, Application US/09982172

Patent No. US20020137119A1

GENERAL INFORMATION:

APPLICANT: EMIL ISRAEL KALZ

TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: Patentin version 3.1

SEQUENCE OF METERS OF SEQ ID NOS: 253

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OTHER INFORMATION: Computer generated synthetic peptide
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; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-81
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; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-83
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Pred. No. 0;
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Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
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SEQ ID NO 80
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ORGANISM: Artificial sequence
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Hyroliberin - eastern newt (tentative sequence)
CjSpecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
CjSpecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
CjSpecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
CjAccession: A9271; A01415
R;Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brai A;Reference number: A92971; MUID:75035605; PMID:4214528
A;Reference number: A92971; MUID:75035605; PMID:4214528
A;Reference number: Drotein
A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI>A;Residues: 1-3 <GRI
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Gaps

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Indels

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Cispecies: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A43391
S;Lackey, D.B.
J. Biol. Chem. 267, 17508-17511, 1992
A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-7
A;Reference number: A43391, MUID:92388092; PMID:1517203
A;Accession: A43391
A;Molecule type: protein
A;Residues: 1-3 claco
C;Keywords: amidated carboxyl end; pyroglutamic acid
C;Keywords: amidated carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: S13894
R;Nagai, A.; Scheidegger, A.
Arch. Biochem. Bloophys. 284, 127-132, 1991
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage. A;Reference number: S13894; MUD:91112783; PMID:1989490
A;Reference protein
A;Residues: 1-3 <NAG>
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C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
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                                  A,Accession: PQ0010
A,Molecule type: protein
A,Residues: 1-3 <MAR>
A,REsidues: angiotensin-converting enzyme inhibitor
C,Keywords: angiotensin-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.0%; Score 0; DB 3; Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches
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Best Local Similarity 0.0%;
Matches 0; Conservative
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Best Local Similarity 0.0%;
Matches 0; Conservative
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   A; Reference number: PQ0008
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NyAlternate names: ficus latex peptide 3
C;Species: Ficus carica (common fig)
C;Date: 15-Unn-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PQ0010
E;Accession: PQ0010
A;Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
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A22565
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri)
C.Species: Gastroclonium coulteri
C.Species: Gastroclonium coulteri
C.Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C.Accession: A22565
R.Klotz, A.V. Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A,Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: A22565
A;Molecule type: protein
A;Residues: 1-3 <KLO>
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
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0; Mismatches
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Best Local Similarity 0.04
Matches 0; Conservative
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PT0636
T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
C;paccies: Mus musculus (house mouse)
C;paccies: Mus musculus (house mouse)
C;paccies: Mus musculus (house mouse)
C;paccies: Dan-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0636
K;Péeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Accession: PT0636
A;Accession: PT0636
A;Accession: PT0636
A;Accession: PT0636
A;Accession: PT0636
A;Accession: PT0636
A;Accession: Translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-3 <PEE>
A;Residues: 1-2 <PEE>
A;Residues: T-2 <PEE>
A;Residues: T-2 <PEE>
A;Residues: T-2 <PEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tiell receptor beta chain V-D-J region (141-1BD) - mouse (fragment)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Insumerulus (house mouse)
Cispecies: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
Cispecies: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
Cispecies: Freency, A.J.
J. Exp. Med. 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A.Reference number: PT0509; MUID:91277601; PMID:1711558
A.Reference number: PT0509; MUID:91277601; PMID:1711558
A.Residue: translation not shown
A.Molecule type: mRNA
A.Residues: 1-3 FEEA
A.Residues: 1-3 FEEA
A.Residues: 1-3 FEEA
A.Residues: 1-3 FEEA
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C;Species: Mns musculus (house mouse)
C;Species: Mns musculus (house mouse)
C;Accession: PT0571
R;Feeney, A.J.
B;Feeney, A.J.
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0571
A;Accession: PT0571
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Residues: Translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 *PEB>
A;Residues: 1-3 *PEB>
A;Residues: 1-3 *PEB>
A;Residues: 1-3 *PEB>
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Cybecies: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
Cyaccesion: 150412
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Cyaccesion: 150412
AyTitle: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken
AyTitle: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken
AyReference number: A6643; MUID:93216790; PMID:8463325
AyAccession: 150412
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Cispecies Bothrops insularis (island jararaca)

Cispecies 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

Cipate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

Cipate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

Richtera A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protesin Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Status: preliminary
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
J. Protein Chem. 9, 221-227, 1990
J. Protein Chem. 9, 221-227, 1990
J. Protein Chem. 9, 221-227, 1990
J. Protein Chem. 9, 221-227, 1990
J. Protein Chem. 9, 221-227, 1990
J. Reference number: A37196; MUID:90351557; PMID:2386615
J. Accession: B37196
J. Accession: Dreliminary
J. Molecule type: protein
J. Section: J. 3 cIIN
J. Residues: 1-3 cIIN
C; Reywords: pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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A;Molecule type: protein
A;Residues: 1-3 <CIN>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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Matches 0; Conservative 0; Mismatches
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tyrosine protein kinase - mouse (fragment)

(Species: Nus musculus (house mouse)

(Species: Nus musculus (house mouse)

(Species: Nus musculus (house mouse)

(Species: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

(Species: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

(Species: 17-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

(Species: 17-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

(Species: Nus musculus in 1889

A; Reference number: 158407; MUID: 95060800; PMID: 7970703

A; Accession: 178890

A; Accession: 178890

A; Accession: 178890

A; Accession: 178890

A; Cross-references: GB:L33339; NID: 9609536; PIDN: AAA64432.1; PID: 9609538

C; Genetics:

A; Gene: p52ntk
                                                                                                                                                                                             T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: IS-Jun-2001 #sequence revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0622; PT0680; PT0582; PT0673
R;Feeney, A.J.
J; Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0609; MUID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Molecule type: DNA
A)Residues: 1-3 <FES1>
A)Experimental source: day 18 fetal thymus, strain BALB/c clones 154-1J and 154-1F
A)Accession: PTO582
A)Accession: PTO582
A)Molecule type: mRNA
A)Residues: 1-3 <FES2>
A)Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2A
C)Keywords: T-cell receptor
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A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Xperimental source: newborn thymus, strain BALB/c, clone 111-1P
A;Accession: Pr0680
A;Status: translation not shown
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Sequence:

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SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.

TISSUB-Optic lobe;
MEDLINE=98100358; PubMed=9437704;
Henry J., Favrel P., Boucaud-Camou E.;
Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related peptide inhibiting the motility of the mature oviduct in the cuttlefish, Sepia officinalis.";
Peptides 18:169-144(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i-FUNCTION: Regulatory neuropeptide with myotropic activity targeting the distal oviduct. Inhibits the motility of the oviduct by decreasing tonus, frequency and amplitude of contractions.
-i-SUBCELLUIAR LOCATION: Secreted.
-i-MASS SPECTROMETRY: MW=259.9; METHOD-WALDI; RANGE=1-2; NOTE=Ref.1. Amidation; Direct protein sequencing; Neuropeptide.
MOD RES
2 1 Tryptophan amide.
SEQÜENCE 2 AA; 261 MW; 737810000000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Neuropeptide GWa.
Sepia officinalis (Common cuttlefish).
Eukaryota, Metazoa; Mollusca, Cephalopoda; Coleoidea; Neocoleoidea;
NCBI_TAXID=6610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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GRAW HUMAN
STANDARD; PRT; 3 AA.
PO115;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Growth-modulating peptide.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0;
0; Mismatches
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PRCT PERAM
PSK DAUCA
RE11 LITRU
RE21 LITRU
RE31 LITRU
RE32 LITRU
SUGA ACHOO
TPIS CANFA
TRM3 ECOLI
UC22 MAIZE
UF01 MOUSE
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MBDLINE=77162369; PubMed=858356;
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                                                                                                                                                               December 29, 2004, 21:01:44 ; Search time 185 Seconds (without alignments) 24.881 Million cell updates/sec
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                               te for the lux operon.";

Bacteriol. 172:679-6802 (1990).

Bacteriol. 302-6802 (1990).

FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It is a component of the fatty acid reductase complex responsible for converting tetradecanoic acid to the aldehyde which serves as substrate in the luciferase-catalyzed reaction.

- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.

- PATHWAY: Bioluminescent fatty acid reduction system; second step.

- SIMILARITY: Belongs to the luxE family.
                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Iong-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
                                                                                                                            Gaps
                                 to stimulate
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=91072226; PubMed=2254256;
Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
"A new Vibrio fischeri lux gene precedes a bidirectional termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
        "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
Experientia 33:324-325(1977).
-!- MISCELLANBOUS: This serum tripeptide has been found to stimular
growth of some cell types and to inhibit other types in vitro.
GO; GO:0001558; P:regulation of cell growth; NAS.
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                                                                  Direct protein sequencing. SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;
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                                                                                                               llarity 0.0%; Pred. No. 0;
Conservative 0; Mismatches
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0; Mismatches
Schlesinger D.H., Pickart L., Thaler M.M.;
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                                                                                                                                                                                                                                                                                                     protein synthetase) (Fragment)
                                                                                                    0.0%;
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tes 0; Conserv
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ID _THYL_PIG
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Characterization of ovine hypothalamic hypophysiotropic TSH-releasing
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MEDLINE=75035605; PubMed=4214528;
Grimm-Oergansen Y., McKelvy J.F.;
Grimm-Oergansen Y., McKelvy J.F.;
Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";
J. Neurochem. 23:471-478(1974).
J. Neurochem. 23:471-478(1974).
In the anterior pituitary gland and as a neurotransmitter/
neuromodulator in the central and peripheral nervous systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ward D.N.; "The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone releasing factor of ovine origin by means of mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thyrotropin
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
11-YDU-10104 (Rel. 44, Last annotation update)
5-JUL-2004 (Rel. 44, Last annotation update)
Subserin (Thyrotropin releasing hormone) (TRH) (Protirelin).
Ovis aries (Sheep),
Bombina orientalis (Oriental fire-bellied toad), and
Norophthalmus viridescens (Eastern newt) (Triturus viridescens).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V., "The identity of chemical and hormonal properties of the thys realeasing hormone and pyroglutamyl-histidyl-proline amide."; Biochem. Biophys. Res. Commun. 37:705-710(1969).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.; "Structure of porcine thyrotropin releasing hormone."; Biochemistry 9:1103-1106(1970).
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Yasubara T., Nakajima T.;
"Occurrence Pyr-His-Pro-NH2 in the frog skin.";
Chem. Pharm. Bull. 23:3301-3303(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 Proline amide.
380 MW; 7761F6B000000000 CRC64;
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MEDLINE=70039904; PubMed=4982117;
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MEDLINE=70163386; PubMed=4985794;
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dioxide.
-!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
-!- COPACTOR: Binds I copper(I) ion, I molybdenum(VI) ion and I molybdepterin cytosine dinucleotide (MCD) per subunit.
-!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
                                                                                                                                                                                       Kraut M., Hugendieck I., Herwig S., Meyer O.,
"Homology and distribution of CO dehydrogenase structural genes in
carboxydetrophic bacteria.",
Arch. Microbiol. 152:335-341(1989).
                                                                                                                                                                                                                                                           -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
                                                    Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae.
NCBI_TaxID=290;
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) dehydrogenase subunit L) (CO-DH L) (Fragment).
Name=cutL;
                                                                                                                                                                                                                                                                                                                                                                                                               protein sequencing; Molybdenum; Oxidoreductase.
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red. No. 0;
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0; Mismatches
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MEDLINE=90055678; Pubmed=2818128;
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MEDLINE=90055678; PubMed=2818128;
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0; Conservative
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Best Local Similarity 0.00
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P19918;
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-1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency and produces a spike broadening of the identified heart excitatory neuron (PON); also enhances the amplitude and frequency of the heart beat. Has also an effect on several other muscles.
PIR; A32480; A32480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-3014529; PubMed-1399265; Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H., Iwashita T., Nomoto K.; Iwashita T., Nomoto K.; Prestal structure and molecular conformation of achatin-I (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid
                                                                                                                                                                                                                                                                                               Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Ferussac; TISSUE=Ganglion; MBDLINE=89273551; PubMed=2597281; Ramatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K., Kunaee K., Sun X.P., Yongaixi A., Kim K.H., Novales-Li P., Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.; Andapi C.G., Takeuchi H., Nomoto K.; In an endogenous neuroexcitatory tetrapeptide from Achatina Eulica Ferussac containing a D-amino acid residue."; Biophys. Res. Commun. 160:1015-1020(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Ferussac; TISSUE=Heart atrium; MEDINE=91264856; PubMed=1675569; Pulimoto K., Kalora I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.; Purification of achatin-I from the atria of the African giant snail, Achatina fulica, and its possible function."; Biophys. Res. Commun. 177:847-853(1991).
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MOD_RES 2 2 D-phenylalanine.

SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
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(Rel. 44, Last annotation update)
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01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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0.0%; Pred. No. 0;
:ive 0; Mismatches
                         0; Mismatches
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         Pred. No. 0;
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Gaps

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Length 4;

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--- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
--- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
--- SUBJUNIT: Heterotrimer consisting of a large, a medium and a small
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Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                      Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to carbon
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                                               01-FEE-1991 (Rel. 17, Created)
01-FEE-1991 (Rel. 17, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO dehydrogenase subunit S) (CO-DH S) (Fragment).
                                                                                                                                                                                                              Pseudomonas carboxydohydrogena.
Bacceria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae.
NCBI_TaxID=290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide
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Pred. No. 0;
0; Mismatches 1; Indel
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MEDLINE=93391436; PubMed=8397415;
McFarlane I.D., Hudman D., Nochacker H.-P., Grimmelikhuijzen C.J.P.;
"The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-Klamide.";
Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle proups. May be involved in the expansion phase of feeding behaviour in sea anemones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92195954; PubMed=1686933;

Bvans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Tidentification of RPamide neuropeptides in the medicinal leech.";

Peptides 12:897-908(1991).

-1- SUBCELLULAR LOCATION: Secreted.

-1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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                                                                                                                                                                                                                                                                                                                                                    FMRFamide-like neuropeptide YMRF-amide.
Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinidae; Hirudinida
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Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
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-!- SUBCELIULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron specific.
PIR; JQ1273; JQ1273.
Amidation; Direct protein sequencing; Neuropeptide.
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MOD_RES 4 4 4 Phenylalanine amide.
SEQUENCE 4 AA; 616 MW; 69D4068B3000000 CRC64;
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                                                                                                                                                                                                                                                                                   (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 44, Last annotation update)
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Pred. No. 0;
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Best Local Similarity 0.0%;
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-I- MISCELLANEOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.

GO: GO:0006935; P:chemotaxis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goetzl B.J., Austen K.F.; "Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of
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Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Indentification of Remide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
FMRFamide-11ke neuropeptide YLRF-amide.
Hirudo medicinalis (Medicinal leech).
Hirudo medicinalis (Medicinal leech).
Arhynchobdellida; Annelida; Clitellata; Hirudinida; Hirudinea;
NCBI_TAXID=6421;
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MOD RES

4 4 Phenylalanine amide.

SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Eosinophilotactic peptides.
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Best Local Similarity 0.0%;
Matches 0; Conservative
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"Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc."; Prep. Biochem. 7:261-281(1977).
Reinscheid R.K., Nothacker H.-P., Staley A.L.; "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea anemone neuropeptide containing an unusual amino-terminal blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.; "FMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                   Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Neuron specific.
--- MASS SPECIFORTRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
--- AMAS A35779; A35779.
--- Amidation; Direct protein sequencing; Neuropeptide.
--- MOD_RES
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"Identification of RFamide neuropeptides in the medicinal leech.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
Veneroidea; Veneridae; Macrocallista.
NCBI_TaxID=6594, 6353, 6421, 27815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure of a molluscan cardioexcitatory neuropeptide."; Science 197:670-671 (1977).
                                                                                                                                                                                                                                                                                   1; Indels
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
FWRFamide (Peak C) (Cardioexcitatory neuropeptide)
Macrocallists nimbosa (Sun-ray clam),
Macrocallists virens (Sandworm),
Hirudo medicinalis (Medicinal leech), and
Helisoma trivolvis (Snail).
                                                                                                                                                                                             4 4 A Asparagine amide.
4 AA; 549 MW; 64540729A0000000 CRC64;
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MEDLINE=94286417; PubMed=7912428;
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MEDLINE=78012038; PubMed=909875;
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MEDLINE=92195954; PubMed=1686933;
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MEDLINE=90259866; PubMed=2342992;
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nes 0; Conservative
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MEDLINE=94286417; PubMed=7912428;
Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FMRFamide-related peptides from the kidney of the snail, Hellsoma
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Sanns B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Idantification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Actiniaria,
Nynantheae, Actiniidae, Anthopleura.
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MEDLINE=90319122; PubMed=1973541;
Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff
                                                                                                         1; Indels
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Amidation; Direct protein sequencing; Neuropeptide.
MOD_RES 4 4 Phenylalanine amide.
SEQÜENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;
                     Alanine amide.
6DD339C9A0000000 CRC64;
   3-phenyllactic acid.
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(Rel. 32, Last sequence update)
(Rel. 44, Last annotation update)
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05-JUL-2004 (Rel. 44, Last annotation update)
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DT 28-FEB-2003
DT 05-JUL-2004
DE Antho-RNamid
OS Anthopleura
OC Nynantheae;
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RP SEQUENCE, AR
RX MEDLINE=9031
RA Grimmelikhui
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        Peptides 15:31-36 (1994).

-!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological activities include augmentation, induction, and regularization of cardiac contraction.

-!- SUBCELMULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the PARP (FWRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=92270459; PubMed=1821096;
Nothacker H.-P., Rinchart K.L. Jr., McFarlane I.D.,
Ctimmelikhuijzen C.J.P.;
"Isolation of two novel neuropeptides from sea anemones: the unusual,
biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-
phenyllactyl fragment Tyr-Arg-Ile-NH2.";
peptides 12:1165-1173 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91391416; PubMed=8397415; McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.; McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.; "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Kamide and Antho-Riamide."; Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding
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Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nymantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
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PIR; A60418; A60418.
Andation; Direct protein sequencing; Neuropeptide.
MOD RES.
SEQÜENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;
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Amidation; Direct protein sequencing; Neuropeptide.
CHAIN 1 4 Antho-Riamide I.
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4 4 180leucine amide.
4 AA; 598 MW; 60441B59A0000000 CRC64;
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Scoring table:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= OTHER
/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
defined)"
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AAB91892
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ABB66810
AAG98134
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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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Length 1;

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New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.
                                                                                        /label= OTHER
/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
defined)"
                               platelet aggregation inhibitor; guanidino group; amidino group.
          Platelet aggregation inhibitor peptide #137.
                                                                                                                                                                                                                                                                                                     Disclosure; Page 10; 34pp; Japanese
                                                                     Location/Qualifiers
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
defined)"
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          0; Mismatches
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Takiguchi Y;

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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
defined)"
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0; Mismatches
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The invention describes peptides of amino acid sequence (1) and their salts. (1) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (1) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
defined)"
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Pred. No. 0;
0; Mismatches
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 Disclosure; Page 10; 34pp; Japanese.
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                                                                                                                                    New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.
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New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.
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ilarity 0.0%; Pred. No. 0;
Conservative 0; Mismatches
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(YAWA ) NIPPON STEEL CORP.
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
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Pred. No. 0;
0; Mismatches
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                                                                    ADD94991 standard; peptide; 1 AA.
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                                                                                      ADD94991;
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The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
defined)"
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
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platelet aggregation inhibitor; guanidino group; amidino group.
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                                                                                                                 New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.
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/note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
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Modified-site
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22-JUN-1994;
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The invention describes peptides of amino acid sequence (I) and their
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
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Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: White, John P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212)664-0525
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APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
US-08-801-092-10
US-08-801-092-17
US-08-801-092-24
US-08-801-092-34
US-08-801-092-38
US-09-298-017-23
US-09-298-017-23
US-09-392-979A-23
US-09-392-979A-23
US-09-103-663-16
US-09-117-927-5
US-09-117-927-5
US-09-117-927-5
US-09-315-113-10
US-09-315-113-17
US-09-315-113-17
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/07820154A Patent No. 5382425 GENERAL INFORMATION:
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TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 57:
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Best Local Similarity 0.0%
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-07-791-213D-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 X 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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APPLICANT: KANAMORI, Toshinori
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
NUMBER OF SEQUENCES: 108
ADDRESSEE: BUTTB, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
                                                                                                                       POLYPEPTIDE, DNA FRAGMENT ENCODING THE SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF TREATING USING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOSTWARE: Patentin Release #1.0, Version #1.25
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY AGENT INFORMATION:
NAME: Meuth, Donna M
REFERENCE/DOCKET NUMBER: 029650-032
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-620
TELEPHATION FOR SEQ ID NO: 24:
SEQUIBNICE CHARACTERISTICS:
                                                                                                                                TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMEN
TITLE OF INVENTION: SAME AND PROCESS FOR PRO
TITLE OF INVENTION: INHIBITION PROCESS, DRUG
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-791-213D-40
; Sequence 40, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
Sequence 24, Application US/07791213D Patent No. 5409895
GENERAL INFORMATION:
                                                                 APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, TOShinori
APPLICANT: NOBUHARA, Masahiro
                                                                                                                                                                                                                                                                                                     CITY: Alexen.
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virginia
: United States
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Best Local Similarity 0.0%
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alexandria
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STATE: Vi
COUNTRY:
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Gaps
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US-08-174-365A-57

Sequence 57, Application US/08174365A

Patent No. 2478809

GENERAL INFORMATION:

APPLICANT: Sedichi TANIDA et al.

TITLE OF INVENTION:

APPLICANT: Sedichi TANIDA et al.

TITLE OF INVENTION:

APPLICANT: Sedichi TANIDA et al.

TITLE OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READBLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parent BW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: UP 2-306745
FILING DATE: 13-NOV-1990
ATTOMNEY/AGENT INFORMATION:
NAME: MAUCH, DORNA M
REGISTRATION NUMBER: 36.607
REFERENCE/DOCKET NUMBER: 029650-032
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 0; DB 1;
bred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0;
0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/1
FILING DATE: December 28, 1
CLASSIFICATION: 514
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NAME: Warren M. Cheek, J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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; INDIVIDUAL ISOLATE: peptide fragment used in the claims US-07-789-913-23
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ORIGINAL SOURCE:
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US-07-789-913-25
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                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Pox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Yamashiro, Donald H.
ITILE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: 1schemia-Related Neuronal Damage
                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                    Length 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN BATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 1991112
FILING DATE: 1991112
PRIOR APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTONNEY/AGENT INPORMATION:
NAME: STARATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
REBERENCE/POCKET UNBER: 365-0005.30
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
LENGTH: 1 amino acids
LENGTH: 1 amino acids
                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Law Offices of Peter Dehlinger
350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                  Query Match
0.0%; Score 0; DB 1
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/07789913 Patent No. 5559095
                                                                                             FEATURE:
NAME/KEY: modified site
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                    LENGTH: 1 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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; INDIVIDUAL ISOLATE: peptide fragment used in the claims
US-07-789-913-25
                                                                                                                                                                                                                                                                                                           APPLICANT: Mijanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Valentino, Karen L.
APPLICANT: Valentino, Karen L.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing TITLE OF INVENTION: 1schemia-Related Neuronal Damage CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                           1; Indels
Length 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC compatible
COMPUTER: Data For Data
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-AUG-1990
ATTORNEY/AGENT INFORMATION:
NUMBE: STIAFICHON-1889
ATTORNEY/AGENT INFORMATION:
NUMBE: STIAFICHON-1889
ATTORNEY/AGENT INFORMATION:
NUMBE: STIAFICHON-1889
DB 1;
0;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Law Offices of Peter Dehlinger STREET: 350 Cambridge Avenue, Suite 300 CITY: Palo Alto
Score 0; DB 1
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    Sequence 25, Application US/07789913
Patent No. 5559095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0%;
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Best Local Similarity 0.0%
Matches 0; Conservative
Query Match
Best Local Similarity 0.04
Matches 0; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
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Sequence 12, Application US/08433037

Sequence 12, Application US/08433037

Patent No. 5707828

GENERAL INFORMATION:
APPLICANT: Barr, Kathryn A.
APPLICANT: Barr, Kathryn A.
APPLICANT: Brierley, Russell A.
APPLICANT: Trachopp, Juerg F.
TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREF: New York
COUNTRY: U.S.A.
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONOPEPTIDE GROUP 1 FRAGMENT, PAGE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                         METHODS OF PRODUCING ANALGESIA AND ENHANCING OPIATE ANALGESIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1;
                                                                                                                                                                                                                                              COMPUTER: USA

ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/POCKET NUMBER: 34,444
REFERENCE/POCKET NUMBER: 365-0009.30
TELECOMMUTICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 mainto acids
TITLE OF INVENTION: METHODS OF PRODUCING ANAL TITLE OF INVENTION: METHODS OF PRODUCING ANAL TITLE OF INVENTION: ENHANCING OPIATE ANALGESI. NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Law Offices of Peter Dehlinger STEET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 0; DB 1;
Pred. No. 0;
0; Mismatches
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0; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 0; Conserv
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                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                   APPLICANT: SUSILLE, ALLANDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: WALENTINO, KAREN L
APPLICANT: WILJANICH, GEORGE P
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA AND
TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONOPEPTIDE GROUP 1 FRAGMENT, PAGE 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/049,794

FILING DATE: 19930415

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/814,759

FLING APPLICATION DATA:

APPLICATION NUMBER: US 07/814,759

FLING APPLICATION NUMBER: S676-1091

ATTORNEY/AGENT INFORMATION:

REGISTRENCE/DOCKET NUMBER: 5865-0009.30

TELEPHONIS: (415) 324-0960

INFORMATION FRORMATION:

TELEPHONE: (415) 324-0960

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHRACTERISTICS:

LENGTH: 1 amino acids

TOTALE CONTINUM ACIDS

TOTALE CONTINUM ACIDS

TELEFAT.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
                                                                                                                                                                   Sequence 23, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
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Best Local Similarity 0.04
Matches 0; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
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INDIVIDUAL ISOLATE:
US-08-049-794-23
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                                                                                                                                                   US-08-049-794-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
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(202)331-7111
    TELEPHONE:
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STATE: VI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-869-933-16
                                                                                                                                                                  US-08-448-606-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Abrahams n, Lars
APPLICANT: Hologren, Erik
APPLICANT: Kalder n, Christina
APPLICANT: Lake, Mats
APPLICANT: Lake, Mats
APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
TITLE OF ENVENTION: Apolipoprotein Al-M
             COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DIG391A0, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
RELEFRANCE/LOCKET NUMBER: 91082
TELEFROWER (516) 742-4346
TELEFROME (516) 742-4366
TELEFROME (516) 742-4366
TELERY: CASE OF SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.0%; Score 0; DB 1; Best Local Similarity 0.0%; Pred. No. 0; Matches 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TREET: 1990 M Street, N.W., Suite 800 STATE: D.C. COUNTRY: U c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0151/00121
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FILING DATE: 1.-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amernick, Burton A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-448-606-4
Sequence 4, Application US/08448606
; Patent No. 5721114
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REFERENCE/DOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pollock, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                          amino acid
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TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
TITLE OF INVENTION: IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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Pred. No. 0;
0; Mismatches 1; Indels
                                                                                                                                                                                    Score 0; DB 1; Length 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
                                                                                                                                                                                                       Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-293-150A-24 ; Sequence 24, Application US/08293150A
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET NUMBER: 4031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29,768
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                                                                                                                                                                                  Query Match
Best Local Similarity 0.0%; I
Matches 0; Conservative (
TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 0.0*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-07-869-933-16
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ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-293-150A-40
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Patent No. 5792629
GENERAL INFORMATION
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, TOSHINOTI
APPLICANT: NOBURARA, MOSABITO
TITLE OF INVENTION: DALVPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
CORRESPONDENCE ADDRESS: 110
CORRESPONDENCE ADDRESS: GREAT OF SECURAL SAME AND STREET: P.O. BOX 1404
                               APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
TITLE OF INVENTION: TREATING USING THE SAME
CORRESPONDENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                   STREET: P.O. BOX ATTOR
CITY: Alexandria
STATE: Virginia
STATE: Virginia
STATE: Virginia
CONTRY: United States
ZIN: 22313-1404
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION TOWNER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION NUMBER: 36,607
FILING DATE: MOWNER: 36,607
FILING DATE: (703) 836-6620
TELECOMMUNICATION INFORMATION:
TELEPAN: (703) 836-2021
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LANDER: Amino acide
TWOST. AMINORMATICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0;
0; Mismatches
MORISHITA, Hideaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.0%;
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US-08-293-150A-40
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APPLICANT:
APPLICANT:
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US-08-496-847-25
US-08-496-847-25
Sequence 25, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
APPLICANT: Amsturz, Gary A.
APPLICANT: Gohlin, Kishorchandra
APPLICANT: Adriaenssens. Peter I.
APPLICANT: Adriaenssens. Peter I.
APPLICANT: Adriaenssens. Peter I.
APPLICANT: Adriaenssens. Peter I.
APPLICANT: Adriaenssens.
ITILE OF INVENTION: METHODS AND
ITILE OF INVENTION: PORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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                                                                                                                                                             LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: 11near
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: US
ZIP: 94306-1546
COMPUTER: READDALE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGRNT INFORMATION:
NAME: STRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELEPHONE: 650-324-0860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
REGISTRATION NUMBER: 34,444
REFREENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
INFORMATION FOR SEQ 1D NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ర
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0.0%; Score 0; DB 1; Length 1;

Query Match

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Sequence 211, Apsequence 395, Asequence 611, Asequence 611, Asequence 111, Asequence 111, Asequence 184, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Asequence 186, Aseque

Sequence 1045,

any residue except Arg, Cys, Met, Phe, Trp. Val

LOCATION: (4)...(4)
OTHER INFORMATION: Xaa is
OTHER INFORMATION: Tyr or

Regult No.

Sequence 500, Sequence 744, Sequence 325,

OM protein

Run on:

Sequence:

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OTHER INFORMATION: polypeptide motif

NAME/KEY: VARIANT

LOCATION: (2)...(2)

OTHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,
OTHER INFORMATION: Pro, Trp or Val

NAME/KEY: VARIANT

LOCATION: (3)...(3)

OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or Pro

NAME/KEX: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09778885

Publication No. US20020039748A1

GENERAL INNORMATION:

APPLICANT: Conklin, Darrell C.

APPLICANT: Conklin, Darrell C.

APPLICANT: Gao, Zeren

TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS

TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS

TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS

TITLE OF INVENTION: AND METHODS FOR MAKING IT

FILE REFERENCE: 98-22

CURRENT PAPLICATION NUMBER: US/09/778,885

CURRENT FILING DATE: 1990-05-26

PRIOR APPLICATION NUMBER: US 60/087,032

PRIOR FILING DATE: 1998-05-26

PRIOR FILING DATE: 1998-05-26

PRIOR FILING DATE: 1998-05-28

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 51
9 US-09-982-172-81

9 US-09-982-172-83

9 US-09-982-172-86

9 US-09-982-172-93

9 US-09-982-172-105

9 US-09-982-172-105

9 US-09-982-172-112

9 US-09-982-172-112

9 US-09-982-172-112

105-09-982-172-148

105-09-982-172-160

105-09-982-172-160

105-09-982-172-160

105-09-982-172-173-105

105-09-982-172-173-105

105-09-982-172-191

105-09-982-172-191

105-09-982-172-195

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105-09-882-171-611

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105-09-882-171-611

105-09-883-245-186

105-09-883-245-186

105-09-883-245-186

105-09-883-245-186

105-09-883-245-186
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                     0000000000
                                                               00000000000000000000000000
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             Sequence 5, Applisequence 4, Applisequence 4, Applisequence 4, Applisequence 1, Applisequence 11, Applisequence 11, Applisequence 31, Applisequence 35, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Applisequence 60, Appliseq
                                                                                                                                December 30, 2004, 13:08:04; Search time 59.6226 Seconds (without alignments) 48.267 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-909-348-4
US-09-982-172-4
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US-09-982-172-11
US-09-982-172-11
US-09-982-172-13
US-09-982-172-31
US-09-982-172-31
US-09-982-172-34
US-09-982-172-34
US-09-982-172-36
US-09-982-172-36
US-09-982-172-46
US-09-982-172-46
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                1599051 seqs, 359727711 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
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8
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Minimum DB Maximum DB

Database

Searched:

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GENERAL INFORMATION:

APPLICANT: Carney, Darrell H.

APPLICANT: Carney, Darrell H.

APPLICANT: Stiernberg, Janet

APPLICANT: Stiernberg, Janet

APPLICANT: Stiernberg, Janet

APPLICANT: Bergmann, John

TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists

TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Rec

FILE REFERENCE: 3003.1003-001

CURRENT APPLICATION NUMBER: US/09/909,348

CURRENT FILING DATE: 2001-07-19

PRIOR FILING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09982172

Patent No. US20020137119A1

GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/2283
CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PATENTIN Version 3.1
LENGTH: 1

LENGTH: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)...(14)
OTHER INFORMATION: Xaa at position six is Glu or Gln
OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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Pred. No. 0;
0; Mismatches 1; Indel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide fragment of Thrombin
NAME/EXY: VARIANT
LOCATION: (1)...(14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.0%; Score 0; DB 9; Best Local Similarity 0.0%; Pred. No. 0; Matches 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 14
                                                                                                                               RESULT 2
US-09-909-1348-4
; Sequence 4, Application US/09909348
; Patent No. US20020042373A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 0.0%
Matches 0; Conservative
       1 X 1
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; OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp, Tyr
US-09-778-885-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCKTHON: (23)
OCHERE INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or Val
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (16).
OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cys, Glu, His or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAMES KEY: VARLANT
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr
OTHER INFORMATION: and Ser
                                                                                                                                                                                                NAMES INFORMATION: Met, Phe or Trp
LOCATION: (5)...(5)
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe, OTHER INFORMATION: Ser, Thr or Trp
NAME/EX: VARIANT
                                                                                                                                     Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (11)...(11)
OTHER INFORMATION: Kaa is any residue except Ala, Cys, Glu, His, Ile,
OTHER INFORMATION: Pro, Trp and Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gly, His,
                                                                              NAME/KEY: VARIANT
COCATION: (6)
CTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser,
OTHER INFORMATION: or Met
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (22)
OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (24)....(24)
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu,
OTHER INFORMATION: or Trp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
LOCATION: (14)...(14)
OTHER INFORMATION: Kaa is any residue except Arg, Asn, Cys,
OTHER INFORMATION: Ser, Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CyB,
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JTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Kaa is any residue except Ala, Asp,
OTHER INFORMATION: Met, Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa is Phe, Tyr, Ile, Trp or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (21)...(21)
OTHER INFORMATION: Xaa is any residue except Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (20)...(20)

JTHER INFORMATION: Xaa is Lys, Asn, Ser or Asp

NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.0%; Score 0; DB 9;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa is Gly or Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: (19)...(19)
OTHER INFORMATION: Xaa is Tyr or Phe
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ... (17)
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
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Gaps

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Gaps

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Gaps

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1; Indels

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APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 19
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Sequence No. US20020137119A1

GRNERAL INFORMATION:

GRNERAL INFORMATION:

GRNERAL INFORMATION:

GRNERAL INFORMATION:

TITLE OF INVENTION:

DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND ANTIBODIES TITLE OF INVENTION:

UTILIZING EACH

FILE REPERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT APPLICATION NUMBER: US/09/982,172

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 253

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-19
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TITLE OF INVENTION: UTILIZING EACH FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
FEATURE:
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US-09-982-172-31
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                                                                                                                 Sequence 4, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: UTRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
TITLE OF INVENTION: UTBECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
TITLE OF INVENTION: UTBECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
TITLE OF INVENTION: UTBECTED THEREAGAINST, AND METHODS, SYSTEMS AND ANTIBODIE
TITLE REFERENCE: 01/22031
CURRENT APPLICATION UNDER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 4
LENGTH: 1
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Secont No. US20020137119A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL

TITLE OF INVENTION: UTILIZING EACH

TITLE OF INVENTION: UTILIZING EACH

FILE REFERENCE: 01/22283

CURRENT APPLICATION NUMBER: US/09/982,172

CURRENT FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253

SOFTWARE: Patentin version 3.1

SEQ ID NO 9
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Patent No. US20020137119A1;
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
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Best Local Similarity 0.0%
Matches 0; Conservative
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US-09-982-172-11
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APPLICANT: Emil Israel Katz
TITLE OF INVENTION: DIRECTED THERESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 69, Application US/09982172
Sequence 69, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATION:
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 69
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; APPLICANT: Emil Israel Katz; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI); TITLE OF INVENTION: UTLIZING EACH
; FILE REFERENCE: 01/22283
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Pred. No. 0;
0; Mismatches
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Pred. No. 0;
0; Mismatches
                                          US-09-982-172-46
Sequence 46, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
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Best Local Similarity 0.0%; I
Matches 0; Conservative C
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Best Local Similarity 0.0%
Matches 0; Conservative
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TITLE OF INVENTION: PRETIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT APPLICATION DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
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APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT
TITLE OF INVENTION: UTILIZING EACH
FILE REFERENCE: 01/2283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT PILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
LENGTH: 1
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                                                                    Length 1;
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US-09-982-172-35
; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-31
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
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                                                                  Score 0; DB 9
Pred. No. 0;
0; Mismatches
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; Patent No. US20020137119A1
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                                                                  Query Match 0.0%;
Best Local Similarity 0.0%;
Matches 0; Conservative
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APPLICANT: Emil Interest Ratz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 83. Application US/09982172

Patent No. US2002013711941

RENERAL INFORMATION:
APPLICANT: Emil lerael Katz

TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIE
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
TITLE OF INVENTION: UTILIZING EACH
FILE REPERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT PILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 83
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                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Computer generated synthetic peptide US-09-982-172-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 0; DB 9;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                               Score 0; DB 9;
Pred. No. 0;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: Patentin version 3.1
SEQ ID NO 80
LENGTH: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 81, Application US/09982172
Patent No. US20020137119A1
                                                                                                                                    TYPE: PRT
ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
FEATURE:
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Best Local Similarity 0.0%;
Matches 0; Conservative
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Matches 0; Conservative
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US-09-982-172-81
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Query Match 0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps

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2b 1 R 1
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Search completed: December 30, 2004, 13:49:58 Job time : 60.6226 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

December 30, 2004, 12:58:17; Search time 9.20755 Seconds (without alignments) 83.598 Million cell updates/sec Run on:

US-10-046-922-32 8 1 XXXXXXX 8 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:* 4 0 6 4 .....

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	ОВ	ΙD	Description
	0	0.0	3	<u>س</u>	RHSHT	thyroliberin - she
7	0	0.0	9	٣	A92971	thyroliberin - eas
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4	0	0.0	æ	٣	A22565	R-phycoerythrin al
S	0	0.0	3	٣	PQ0010	angiotensin-conver
ø	0	0.0	e ,	ო	S13894	histidinol dehydro
7	0	0.0	e	٣	A43391	TRH-like tripeptid
80	0	0.0	e	٣	E37196	bradykinin-potenti
σ	0	0.0	m	m	F37196	bradykinin-potenti
	0	0.0	m	ო	I50412	gene p20K protein
11	0	0.0	m	٣	PT0636	T-cell receptor be
	0	0.0	m	m	PT0578	
13	0	•	ო	m	PT0571	T-cell receptor be
14	0	0.0	ю	ო	PT0622	T-cell receptor be
15	0		Э	m	178890	tyrosine protein k
16	0	0.0	Э	m	S68328	blood cell protein
17	0	•	e	m	T13892	cytochrome-c oxida
18	0		e	m	GKHU	growth-modulating
19	0		m	m	RHPGT	thyroliberin - pig
70	0		e	m	A60898	- chicke
21	0	٠	e	ო	A23751	spinal cord peptid
22	0	•	m	m	B23751	spinal cord peptid
23	0	•	Ю	m	A33802	thyrotropin-releas
24	0		4	Н	ECXAA	antho-RFamide neur
25	0	•	4	~	S18401	thyroglobulin - do
56	0	•	4	0	A02147	
27	0	•	4	~	A37832	oxyg
28	0	0.0	4	7	A48360	gamma subunit of P
53	0	0.0	4	~	A61300	22K superhelical D

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## ALIGNMENTS

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Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cipate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
Cipate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
Cipate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
Ribersiderio Jr., D.M.; Burgus, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
A;Reference number: A93750
A;Reference number: A93750
A;Residues: 1-3 < CDES>
A;Costareferences: UNIPROT: P01151
R;Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
R;Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
A;Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
A;Tetle: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
A;Tote: physicochemical characteristics and biological activities of the natural and synt C;Superfamily: thyroliberin
C;Superfamily: thyroliberin
C;Superfamily: thyroliberin
C;Keywords: amidated carboxylic acid (Gin) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Gin) #status experimental
                                                                                                  thyroliberin - sheep
RESULT 1
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Gaps ö 1; Indels

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Query Match 0.0%; Score 0; DB 3; Length 3; Best Local Similarity 0.0%; Pred. No. 0; Matches 0; Conservative 0; Mismatches 1; Indela

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Cispecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
Cispecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
Cispecies: Notophthalmus viridescens, Triturus viridescens (eastern newt)
Cispace: 15-0un-2001 #sequence_revision 15-0un-2001 #text_change 09-0ul-2004
Cispacession: A52971; Molt415
N. Neurochem. 23, 471-448, 1974
A.Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) branch Ricescence number: A92971; MuID: 75035605; PMID: 4214528
A.Accession: A92971
A.Residues: 1-3 cGRI>
A.Residues: 1-3 cGRI>
A.Residues: 1-3 cGRI>
A.Residues: 1-3 cGRI>
A.Residues: 1-3 cGRI>
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Cisperfamily: thyroliberin
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Cisuperfamily: thyroliberin

us-10-046-922-32.rpr

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A; Reference number: PQ0008
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Cipate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
Cipate: 15-Jun-2001 #sequence_revision 1975
R; Yasubara, T; Nakajima, T;
Chem. Pharm. Bull. 23, 3301-3303, 1975
R; Yasefrence of Pyr-His-Pro-NH-2 in the frog skin.
A; Reference number: A90919; MUID:76138399; PMID:815011
A; Residues: 1-3 < VASS.
A; Andecule type: protein
A; Residues: 1-3 < VASS.
A; Cross-references: UNIPROT:P01151
C; Superfamily: thyroliberin
C; Superfamily: thyroliberin
C; Superfamily: thyroliberin
C; Superfamily: #status experimental
F; J/Modified site: amidated carboxyl end (Pro) #status experimental
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C;Species: Flous carica (common fig)
C;Date: 15-Unr-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PQ0010
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment) C;Species: Gastroclonium coulteri C;Species: Gastroclonium coulteri C;Species: Gastroclonium coulteri C;Species: Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001 C;Accession: A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Chem. 260, 4856-4863, 1885
A;Feference number: A22565; MUID:85182601; PMID:3886644
A;Accession: A22565
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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                                                                       Length 3;
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches
                                                                         DB 3;
                                                                       0.0%; Score 0; DB 3 ilarity 0.0%; Pred. No. 0; Conservative 0; Mismatches
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                                             Query Match
Best Local Similarity
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R.Lackey, D.B.
O. Biol. Chem. 267, 17508-17511, 1992
A.Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-"
A.Reference number: A43391; MUID:92388092; PMID:1517203
                                                                                                                                                                                                                                                                                                                                                                                                                                                       histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Species: Is-dun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: S13894
R;Nagai, A.; Scheidegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A;Reference number: S13894; MUID:91112783; PMID:1988490
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C;Species: bothrops insularis (island jararaca)
C;Decies: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C;Accession: B37196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Medicago sativa (alfalfa)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: A43391
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A, Residues: anidated carboxyl end, pyroglutamic acid
E,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F,3/Modified site: amidated carboxyl end (Pro) #status experimental
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A,Accession: PQ0010
A,Molecule type: protein
A,Residues: 1-3 <AMA>
A,Experimental source: latex
C,Keywords: angiotensin-converting enzyme inhibitor
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                                                                                                                                                                     Score 0; DB 3;
                                                                                                                                                                                         Pred. No. 0;
0; Mismatches
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A,Residues: 1-3 «NAG»
Experimental source: var. capitata
C,Keywords: dimer; NAD; oxidoreductase
                                                                                                                                                               Query Match 0.0%;
Best Local Similarity 0.0%;
Matches 0; Conservative
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Best Local Similarity
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PT0636

C. Secretor beta chain V-D-J region (100-2AT) - mouse (fragment)

C. Species: Ms musculus (house mouse)

C. Species: Ms musculus (house mouse)

C. Accession: PT0636

R. Peeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A. Accession: PT0636

A. Reference number: PT0609; MUID: 91277601; PMID: 1711558

A. Reference number: MNA

A. Molecule type: mRNA

A. Molecule type: mRNA

A. Molecule type: mRNA

A. Residues: 1-3 < PEE>

A. Residues: 1-3 < CC

C. Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0578
B;Feeney, A.J.
B;Feeney, A.J.
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUD:91277601; PMID:1711558
A;Accession: PT0578
A;Accession: PT0578
A;Accession: PT0578
A;Festue: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residnes: 1-3 *PEB>
A;Festue: cranslation of shown
A;Molecule type: mRNA
A;Residnes: 1-3 *PEB>
A;Experimental source: day 19 fetal thymus, strain BALB/C
C;Keywords: T-cell receptor
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C.Species: Ms musculus (house mouse)
C.Species: Ms musculus (house mouse)
C.Species: Is-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C.Accession: PT0571
B.Feney, A.J.
A.Fifee J. M. M. Med. 174, 115-124, 1991
A.Fifle: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A.Reference number: PT0509; MUD:91277601; PMID:1711558
A.Reference number: PT0509; MUD:91277601; PMID:1711558
A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference number: A.Reference 
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Pred. No. 0;
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Matches 0; Conservative 0; Mismatches
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nes 0; Conservative
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Best Local Similarity 0.0%;
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PT0578
            RESULT 11
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C;Species: Bothrops insularis (island jararaca)
C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: F37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J; Protein Chem. 9, 21-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557; PMID:2386615
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

A; Protein Chem. 9, 221-227, 1990

A; Title: Primary structure and biological activity of bradykinin potentiating peptides A; Reference number: A37196; MUD:90351557; PMID:2386615

A; A; Accession: B37196

A; A; Residual bype: protein

A; Molecule type: protein

A; Residuals: 1-3 - CCIN>
C; Keywords: pyroglutamic acid

F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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A;Molecule type: protein
A;Residues: 1-3 <CIN>
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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Pred. No. 0;
0; Mismatches 1; Indel
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0.0%; Pred. No. 0;
ative 0; Mismatches
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Lycosyu

Lycosyu

CyBecies: Mus musculus (house mouse)

CyBecies: Mus musculus (house mouse)

CyDate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

CyAccession: 178890

Rychow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.

Oncogne 9, 3437-3448, 1994

AyItle: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine protein

AyAccession: 178890

AyAccession: 178890

AyBeatence number: 158407; MulD:95060800; PMID:7970703

AyAccession: TyBes

AyAccession: TyBes

AyAccession: TyBes

AyAccession: TyBes

AyAccession: TyBes

AyAccession: TyBes

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 15-Jun-2001 #sequence revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PT0622; PT0680; PT0582; PT0673
R;Feeney, A.J.
J; Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601; PMID:1711558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translation not shown
A;Status: translation not shown
A;Status: translation not shown
A;Experimental source: newborn thymus, strain BALB/c, clone 111-1P
A;Experimental source: newborn thymus, strain BALB/c, clone 111-1P
A;Experimental source: av 10 fetal thymus, strain BALB/c clones 154-1J and 154-1F
A;Experimental source: day 10 fetal thymus, strain BALB/c clones 154-1J and 154-1F
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2A
B;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2A
C;Keywords: T-cell receptor
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                   December 30, 2004, 12:57:52 ; Search time 73.8113 Seconds (without alignments) 62.362 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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332 3433 3443 346 346 347 347 347 347 347 347 347 347 347 347	JUE SUL		2 8 2	natemen 0, 1 X 1 1 X 1 1 G 1	M. HUMAN STANDP GRWM HUMAN STANDP 101157; 21-JUL-1986 (Rel. 01, 21-JUL-1986 (Rel. 01, 05-JUL-2094 (Rel. 44, Growth-modulating per HOMO Sapiens (Human).
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Guillemin R.;
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                          site for the lux operon..;
J. Bacteriol. 172:679-6802(1990).
-!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It is a component of the fatty acid reductase complex responsible for converting tetradecanoic acid to the aldehyde which serves as substrate in the luciferase-catalyzed reaction.
-!- CATALYTIC: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.
-!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
-!- SIMILARITY: Belongs to the luxE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                              Gaps
                                   stimulate
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"A new Vibrio fischeri lux gene precedes a bidirectional termination
Schlesinger D.H., Pickart L., Thaler M.M.;
"Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
Experientia 33:224-325(1977).
-!- MISCELLANBORS: This serum tripeptide has been found to stimula:
growth of some cell types and to inhibit other types in vitro.
GO; GO:0001558; P:regulation of cell growth; NAS.
                                                                                                                                                                                                                                                     01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19)
protein synthetase) (Fragment).
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les 0; Conservative
                                                                     Direct protein sequencing. SEQUENCE 3 AA; 340 MW;
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nes 0; Conservative
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Characterization of ovine hypothalamic hypophysiotropic TSH-releasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-Pig; MEDLINE=70039904; PubMed=4982117; MEDLINE=70039904; PubMed=4982117; Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.; Boler J., Enzmann F., Folkers H., Folkers H., Folkers H., Folkers C.Y., Schally A.V.; Eleasing hormone and pyroglutamyl-histidyl-proline amide."; Biochem. Biophys. Res. Commun. 37:705-710(1969).
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PIR; A99919; RHTDTO.
PIR; A99971; B49971.
PIR; A99750; HASHT.
Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.

Pyrrolidone carboxylic acid.

Pyrrolidone carboxylic acid.

Proline amide.
                                                                                                         Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin). Sus scrofa (Pig), Ovis aries (Sheep), Ovis aries (Sheep), Bombina orientalis (Oriental fire-bellied toad), and Notophthalmus viridescens (Eastern newt) (Triturus viridescens). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodaccyla, Suina, Suidae, Sus. NCBI_TaxID=9823, 9940, 8346, 8316,
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neuromodulator in the central and peripheral nervous systems.
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SPECIES-Sheep; TISSUE-Hypothalamus;
Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=75035605; PubMed=4214528; Grimm-Joergensen Y., McKelvy J.F.; Blosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=Sheep;
MEDLINE=70163386; PubMed=4985794;
Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=Pig; TISSUE=Hypothalamus;
MEDLINE=70136150; PubMed=4984938;
Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
Structure of porcine thyrotropin releasing hormone.";
Biochemistry 9:1103-1106(1970).
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Yasuhara T., NaKajima T.;
"Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
Chem. Pharm. Bull. 23:3301-3303(1975).
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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0.0%; Score 0; DB 1; Length 3;

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dioxide.
-!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
-!- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1
molybdopterin cytosine dinucleotide (MCD) per subunit.
-!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dioxide.
--- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
--- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
---- COFACTOR: Heterotrimer consisting of a large, a medium and a small
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2Fe-25; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;
                                                                                                                                                                                                                                   Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
                                                                                                                                                                                                                                                                                 carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO dehydrogenase subunit S) (CO-DH S) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arch. Microbiol. 152:335-341(1989).
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae.
                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) dehydrogenase subunit L) (CO-DH L) (Fragment). Name=cutL;
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red. No. 0;
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MEDLINE=90055678; PubMed=2818128;
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Matches 0, Conservative
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Best Local Similarity
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P19918;
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-1- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency and produces a spike broadening of the identified heart excitatory neuron (PON); also enhances the amplitude and frequency of the heart beat. Has also enhances the amplitude and frequency of the PIR; A32480; A32480.

D-amino acid; Direct protein sequencing; Hormone.

MOD RES

2

D-phenylalanine.

SEQÜENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Ferussac; TISSUE-Ganglion; MEDINE-89273551; PubMed=2597281; Ramatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K., Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K., Novales E.T., Kan X.P., Yongairi A., Kim K.H., Novales L.I. P., Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.; "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina Eulica Ferussac containing a D-amino acid residue."; Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
                          Gaps
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MEDLINE=93014529; PubMed=1399265;
Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
Iwashita T., Nomoto K.;
"Crystal structure and molecular conformation of achatin I (H-Gly-D-
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                          1; Indels
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Biochem. Biophys. Res. Commun. 177:847-853(1991).
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(Rel. 17, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                     4 AA.
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    Pred. No. 0;
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  Best Local Similarity
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P19916;
01-FEB-1991
01-FEB-1991
05-JUL-2004
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DCML PSECH
ID DCML PS
AC P19916;
DT 01-FEB-
DT 05-JUL-
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4 AA.

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MEDLINE=92195954; PubMed=1686933;

Bvans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Identification of Remide neuropeptides in the medicinal leech.";

Peptides 12:897-908 [1991].

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the PARP (FWRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P., "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones.";
Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
                                                                                                                                                                                                                                   FWRFamide-like neuropeptide YMRF-amide.
Hirudo medicinalis (Medicinal leech).
Eukaryota; Mecazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
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MCFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.,
"The expansion behaviour of sea anemones may be coordinated by
inhibitory neuropeptides, Antho-Khamide and Antho-Rlamide.";
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several musc
groups. May be involved in the expansion phase of feeding
behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Screted.
-!- TISSUE SPECIFICITY: Neuron specific.
PIR; JQ1273; JQ1273.
Amidation; Direct protein sequencing; Neuropeptide.
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Pred. No. 0;
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MOD RES 4 4 Phenylalanine amide.

SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;
                                                                                                                                                                          (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 44, Last annotation update)
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Best Local Similarity
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FFKA ANTEL
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FAR4_HIRME
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-1- MISCELLANBOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.

GO; GO:0006935; P:chemotaxis, IDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=92195954; PubMed=1686933;

Bvans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Identification of RTamide neuropeptides in the medicinal leech.";

Peptides 12:897-908(1991).

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Hirudo medicinalis (Medicinal leech).
Eukaryota, Metazoa, Annelida, Clitellata, Hirudinida, Hirudinea,
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/FIId=VAR 005201.
4 AA: 390 MW; 6B05B65A0000000 CRC64;
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598 MW; 69D4073B30000000 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-JUL-2004 (Rel. 44, Last annotation update)
Eosinophilotactic peptides.
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Pred. No. 0;
0; Mismatches
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tive 0; Mismatches
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Best Local Similarity 0.0%; I
Matches 0; Conservative (
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Price D.A., Greenberg M.J.;
"Purification and characterization of a cardioexcitatory neuropeptide
"From the central ganglia of a bivalve mollusc.";
Prep. Biochem. 7:261-281(1977).
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MEDLINE=94286417; Pubmed=7912428;
Madrid K.P., Price Dracenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
-!- SUBCELIULAR LOCATION: Secreted.
-! TISSUB SPECIFICITY: Neuron specific.
-!- MASS SPECIFOMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
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"Authentic FWRFamide is present in the polychaete Nereis virens.";
Peptides 11:75-77(1990).
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SPECIBS=H.medicinalis;
MEDLINE=59195594; PubMed=1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Identification of Remide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
Reinscheid R.K., Nothacker H.-P., Staley A.L.;
"Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a e
anemone neuropeptide containing an unusual amino-terminal blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
Veneroidea; Veneridae; Macrocallista.
NCBI_TaxID=6594, 6353, 6421, 27815;
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SPECIES-M.nimbosa; TISSUE-Cerebral pedal, and Visceral ganglion;
MEDLINE-77215956; PubMed-877582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Price D.A., Greenberg M.J.; "Structure of a molluscan cardioexcitatory neuropeptide."; Science 197:670-671 (1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 0; DB 1; Length 4;
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P01162;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
PWRFamide (Peak C) (Cardioexcitatory neuropeptide).
Macrocallista nimbosa (Sun-ray clam),
Marris virens (Sandworm).
Hirudo medicinalis (Medicinal leech), and
                                                                                                                                                                                                                                                                                                                                PIR; A35779; A35779.

Amidation; Direct protein sequencing; Neuropeptide.

MOD_RES 1 1 3-phenyllactic acid.

MOD_RES 4 4 Apparagine amide.

SEQÜENCE 4 AA; 549 MW; 64540729A0000000 CRC64;
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MEDLINE=90259866; PubMed=2342992;
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MEDINE-94386417; PubMed-7912428;
Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FMRFamide-related peptides from the kidney of the snail, Helisoma
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Yeans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
peptides 12:897-908(1991).
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Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Actiniaria,
Nynantheae, Actiniidae, Anthopleura.
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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MEDLINE=90319122; PubMed=1973541;
Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
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MOD RES 4 4 Phenylalanine amide.
SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;
                                                Alanine amide.
6DD339C9A0000000 CRC64;
    3-phenyllactic acid.
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01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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ID FLRF HIR
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   trivolvis.";
Peptides 15:31-36(1994).
-!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
-!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
--- activities include augmentation, induction, and regularization of
cardiac contraction.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR: Belongs to the FARP (FWRPamide related peptide)
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Grimmelikhuijzen C.J.P.;
"Isolation of two novel neuropeptides from sea anemones: the unusual, biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its desphenyllactyl fragment Tyr-Arg-Ile-NH2.";
Peptides 12:1165-1173 (1991).
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McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
"The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188 (1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron specific.
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Bukaryota; Metazoa; Chidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
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PIR; A60418; A60418.
Andation; Direct protein sequencing; Neuropeptide.
MOD RES
SEQÜENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Antho-Rlamide I (Contains: Antho-Rlamide II].
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Melanin-c	Melanin-c	Melanin-c	Amino aci	Melanin-c	Melanin-c	Melanin c	Cyclic pe	Fibronect	MAb anti-	Thrombopo	Thrombopo	Molecule	Molecular							
Add24107	Adh27064	Adh27062	Ado44204	Adp22727	Adq26193	Adp71265	Aap91867	Aaw03419	Aaw25669	Aaw09546	Aaw09564	Aaw09565	Aaw35433	Aaw36715	Aaw35432	Aaw36716	Aaw36697	Aaw65945	Aaw57567	
ADD24107	ADH27064	ADH27062	ADO44204	ADP22727	ADQ26193	ADP71265	AAP91867	AAW03419	AAW25669	AAW09546	AAW09564	AAW09565	AAW35433	AAW36715	AAW35432	AAW36716	AAW36697	AAW65945	AAW57567	
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53.8	53.8	53.8	53.8	53.8	53.8	53.8	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	
14	14	14	14	14	14	14	13	13	13	13	13	13	13	13	13	13	13	13	13	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

0000-0000-10000000

## ALIGNMENTS

Gaps

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Length 10; Indels

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The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a deemnosomal cadherin cell adhesion recognition CAR sequence (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polyneptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                                                                                                                                                                                                                                                                                            Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis.
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Pred. No. 1.2e+02;
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  DB 2;
Score 16; DB 2
Pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Desmocollin-1 CAR cyclic peptide 42.
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                                                                                                                                                                                                                              ABB46640 standard; peptide; 10 AA.
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20.0%;
61.5%;
20.0%;
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                     Similarity
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Query Match
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               immune system. Vaccine prepns. contg. the peptide provide protection against infection by AIDS virus. The peptide can also be used in kits for the detection of the AIDS virus and antibodies to the AIDS virus; and as immunogens to elicit monoclonal antibodies. The peptide may be produced by conventional methods of peptide synthesis using solid phase or liquid phase methods. See also AAP71549-56, and EP-249394. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The synthetic peptide is based on the sequence of peptide T, a sub region of HIV gpl20 responsible for binding to brain membrane and human T cells. The peptide may be truncated from either end to remove cysteine residues. The peptide may be used for treatment of chronic fatigue syndrome not associated with HIV infection. The peptide will reduce fatigue, tenaton, anger and confusion and improves cognitive and neuromoter performance. See also AAR28919-42. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide compsns. for treating chronic fatigue syndrome - ameliorate symptoms and improve vigour and cognitive and neuro-motor performance.
                                                                                                                                                                                                                                                                         Gaps
  AIDS virus in monkey, rat and human brain membranes and cells of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    confusion; peptide T; HIV; synthetic; gp 120.
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                                                                                                                                                                                                                                Score 16; DB 1; Length 10;
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                                                                                                                                                                                                                                                    Pred. No. 28;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CFS; fatigue; tension; anger;
human immunodeficiency virus;
                                                                                                                                                                                                                                61.5%;
20.0%;
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AAR28918

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desmosomal cadherin, cell adhesion, CAR sequence, immunosuppressive, cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
                                                                                          Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
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                                                                Desmocollin-1 CAR cyclic peptide 52
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 23; Page 109; 127pp; English.
                                                                                                                                                                                                                                                                                                               Gour BJ;
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                                                                                                                                                                                                                                                                                    (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                27-MAR-2001; 2001WO-IB001400
                                                                                                                                                                                                                                                          27-MAR-2000; 2000US-00535852
                                      30-JAN-2002 (first entry)
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                                                                                                                                                 Synthetic.
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              ABB46650;
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The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a desmosomal cadherin cell adhesion recognition CAR sequence (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polynucisotide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
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                                                                                                                                                                                                                                            Gour BJ;
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Best Local Similarity
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Blaschuk OW, Symonds JM, Gour BJ;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
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                                                                                                              invention relates to modulating agents for inhibiting or enhancing
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                                   Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis.
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                                                                                       Claim 23; Page 109; 127pp; English
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(ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polynucleotide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
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(first entry)

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Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
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                                                                                   Desmocollin-3/4 CAR cyclic peptide 10.
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 ABB47075 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                  cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                           Gaps
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Pred. No. 1.2e+02;
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Score 15; DB 5; Length Lv;
Pred. No. 1.2e+02;
                                         0; Mismatches
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                                                                                                                                                                        ABB46612 standard; peptide; 10 AA.
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           57.7%;
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                                         Conservative
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Query Match
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The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a desmosomal cadherin cell adhesion recognition CAR sequence (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polymucleotide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence or analogue. The modulating agents have immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
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20.0%; Pred. No. 1.2e+02;
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57.7%; 20.0%;

Query Match Best Local Similarity

Best Loc Matches

2; Conservative

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RESULT 10 ABB47075

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inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-18; cadherin-12; cadherin, related neuronal receptor; LI-cadherin; protocadherin; desmoglein; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                           The present peptide, which binds the thrombopoietin receptor (TR), can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematogical disorders and thrombopoietin agonist, preferably haematogical disorders and thrombocytopaenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
               CM, Johnson SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3644.
                                                                                           Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor – useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulation; nonclassical cadherin mediated cell adhesion; CAR;
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Pred. No. 4.8e+02;
0; Mismatches 8; Indels
               Cwirla SE, Duffin DJ, Gates C
PJ, Wagstrom CR, Wrighton NC;
                                                                                                                                                              Disclosure; Page 27; 106pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY64329 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blaschuk OW, Gour BJ, Byers S;
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99US-00234395.
99US-00264516.
                                                                                                                                                                                                                                                                                                                                                                                53.8%;
20.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
               Dower WJ, Barret RW,
Mattheakis LC, Schatz
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
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                                                               WPI; 1997-052226/05.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1998;
20-JAN-1999;
08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9957149-A2
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                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a peptide which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells
                                                                                                                                                                                                                                                                Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
LC, Schatz PJ, Wagstrom CR, Wrighton NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                              Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, espthrombocytopenia resulting from chemotherapy, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopaenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.8%; Score 14; DB 2; Length 10;
20.0%; Pred. No. 4.8e+02;
tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin receptor binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 27; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW36672 standard; peptide; 10 AA.
                                                                                                                             95US-00473604.
95US-00476168.
95US-00478128.
95US-00484090.
95US-00485301.
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95US-00485301.
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                                                                                 96WO-US008998
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                                                                                                                                                                                                                                   GROUP LID
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   Mattheakis LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 AA;
                                                                                                                                                                                                                                 (GLAX ) GLAXO
                                                                                                                                 07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
07-JUN-1995;
                 WO9640189-A1
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                                                                                 05-JUN-1996;
                                                19-DEC-1996,
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Gaps

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98US-00073040

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The present invention describes cadherin modulating agents (MA)

comprising peptides which comprise a nonclassical cadherin cell adhesion

cecognition (CAR) sequence. The MAs can be used for modulating

cecognition (CAR) sequence. The MAs can be used for adulating

conclassical cadherin-mediated functions. They can be used for e.g.

inhibiting adhesion of nonclassical-cadherin expressing cells in a

mammal, enhancing delivery of a drug through the skin of a mammal,

central inhibiting metastasis of a cancer in a mammal, inhibiting

a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting

conclassing cell, preventing or treating obesity in a mammal, stimulating

conclassing vasopermeability in a mammal, enhancing adhesion of

increasing vasopermeability in a mammal, enhancing adhesion of

conclassical cadherin-expressing cells, inhibiting synaptic stability in

a mammal, or preventing pregnancy in a mammal. They can also be used for

cor reducing scar tissue, or enhancing adhesion of foreign tissue in a

mammal. They can also be used for treating e.g. psoriasis, arthritis, age

crelated maculas degeneration, multiple sclerosis and diabetes. The

products can also be used for detection and diabetes. The

conclassical and Asystals and AASJ3188 represent sequences used in

conclassing vasopermeation of the present invariation of the products can also be used for detection and diagnosis and in bioreactors.

AAV6653 to AAV64572 represent specifically claimed peptides, and

conclassing the products of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the 
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                          cadherin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3646
                          New cadherin modulating agents, used for modulating nonclassical canediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14; DB 3; Length 10;
Pred. No. 4.8e+02;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the exemplification of the present invention
                                                                                                                          Claim 102; Page 218; 252pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY64331 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.8%;
20.0%;
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Best Local Similarity
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The present invention describes cadherin modulating agents (MA)

compristing peptides which comprise a nonclassical cadherin cell adhesion

crecognition (CAR) sequence. The MAs can be used for modulating

crecognition (CAR) sequence. The MAs can be used for edge of the conclassical cadherin-mediated functions. They can be used for e.g.

inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug to a tumour in a mammal, reating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting cancer in a mammal, inhibiting cancer in a mammal, inhibiting cancer in a mammal, inhibiting cancer in a mammal, inhibiting cancer in a mammal, inhibiting cancer in a mammal, stimulating concressing vasopermeability in a mammal, enhancing delivery to the contral nervous system, treating a demyelinating dudesion of increasing vasopermeability in a mammal. Heavy can also be used for treating synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age concreased macular degeneration, multiple sclerosis and diabetes. The products can also be used for treating escretosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAX6652 to AAX64572 represent specifically claimed peptides, and the concretion of the company of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the concretion of the co
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                                                                                                                                                                                                                                                                       New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.8%; Score 14; DB 3; L
20.0%; Pred. No. 4.8e+02;
tive 0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                             Claim 102; Page 218; 252pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU25891 standard; peptide; 10 AA.
                                                                                                                      (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                           Blaschuk OW, Gour BJ, Byers S;
                     98US-00187859.
                                                                       99US-00264516.
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                                                                       08-MAR-1999;
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                     06-NOV-1998;
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Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to thy cophilic polymers. The methods are used to treat thrombocytopenia such the due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin consultation and fixed cells, in biological fluids, in tissue homogenates, and cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological fluids, in tissue homogenates, and in purified or natural biological fluids, in tissue homogenates, or situ staining, fluorescence-activated cell sorting, Mestern blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed corporation with additional cytokines
                                                                                                                                                                                                                                         Schatz PJ;
Deprince RB, Podduturi S;
                                                                                                                                                                                                                                                                                                                                                                      Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%; Score 14; DB 4; Length 10; 20.0%; Pred. No. 4.8e+02; tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                      Dower WJ, Barrett RW, Cwirla SE, Gates CM,
Balasubramanian P, Wagstrom CR, Hendren RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Col 21; 128pp; English
                                                                                95US-00478128.
95US-00485301.
96WO-US009623.
96US-00699027.
                                         01-MAR-2000; 2000US-00516704.
                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD.
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                                                                                07-JUN-1995;
07-JUN-1995;
07-JUN-1996;
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26-JUN-2001
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Search completed: December 29, 2004, 21:35:28 Job time : 96.3333 secs